

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2004, 09:51:51 ; Search time 45 Seconds
(without alignments)
1577.591 Million cell updates/sec

Title: US-10-006-922A-12

Perfect score: 1214

Sequence: 1 MRSKXVIEFMKFKVMEG.....EDYIVEQYRTEGRHFL 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

```
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1214	100.0	225	5	Q9U6Y8	09u6y8 discosoma s
2	1085.5	89.4	230	5	Q9GRT7	09gt17 discosoma s
3	793	65.3	221	5	Q9SP04	09sp04 gonolopora t
4	729.5	60.1	232	5	Q9U6Y7	09u6y7 discosoma s
5	690	56.8	225	5	Q963F5	0963f5 montastraea s
6	681	56.1	225	5	Q95UA7	095ua7 montastraea s
7	681	56.1	225	5	Q95UA7	095ua7 montastraea s
8	679.5	56.0	227	5	Q7Z0W4	07z0w4 montastraea s
9	678.5	55.9	227	5	Q962P9	0962p9 montastraea s
10	678.5	55.9	227	5	Q7Z0W5	07z0w5 montastraea s
11	669.5	55.1	234	5	Q7Z0W7	07z0w7 montastraea s
12	668.5	55.1	234	5	Q8T5F2	08t5f2 clavalaria
13	667	54.9	266	5	Q9U6Y3	09u6y3 clavalaria
14	663	54.6	236	5	Q8T6U0	08t6u0 dendronephth
15	655.5	54.0	227	5	Q95VT0	095vt0 montastraea s

17	654.5	53.9	234	5	Q8MU47	08mu47 montastraea s
18	652.5	53.7	225	5	Q7Z0W9	07z0w9 montastraea s
19	639	52.6	224	5	Q8MU48	08mu48 montastraea s
20	631.5	52.0	225	5	Q8T5F1	08t5f1 montastraea s
21	608.5	50.1	231	5	Q8ISF8	08isf8 parascyoni
22	599.5	49.4	225	5	Q8MU48	08mu48 trachyphyll
23	579.5	47.7	259	5	Q8MMA2	08mma2 agaricia fr
24	574	47.3	228	5	Q9GPI6	09gpi6 anemonia su
25	573.5	47.2	235	5	Q8T5F0	08t5f0 scolymia cu
26	570.5	47.0	231	5	Q8T5T8	08t5t8 discosoma s
27	566.5	46.7	239	5	Q8MMA1	08mma1 agaricia ag
28	559.5	46.1	231	5	Q8T5B9	08t5b9 ricordea fl
29	556.5	45.8	227	5	Q9SM86	09sm86 condylactis
30	556.5	45.8	232	5	Q9GPI5	09gpi5 anemonia su
31	556.5	45.8	232	5	Q9G2Z8	09g2z8 anemonia su
32	553.5	45.6	227	5	Q9SM85	09sm85 radiantus
33	551.5	45.4	231	5	Q8T5B8	08t5b8 ricordea fl
34	548.5	45.2	227	5	Q9SM11	09sm11 condylactis
35	546.5	45.0	231	5	Q8MU46	08mu46 ricordea fl
36	530.5	43.7	228	5	Q86LV4	086lv4 radiantus
37	530.5	43.7	234	5	Q8T5F3	08t5f3 scolymia cu
38	529.5	43.6	227	5	Q8MU45	08mu45 condylactis
39	522.5	43.0	225	5	Q8T6T9	08t6t9 radiantus
40	511.5	42.1	229	5	Q8T5E7	08t5e7 condylactis
41	495	40.8	229	5	Q9U6Y6	09u6y6 anemonia ma
42	490	40.4	214	5	Q86LV8	086lv8 meandrina m
43	485.5	40.0	231	5	Q9U6Y4	09u6y4 zoanthus sp
44	485.5	40.0	238	5	Q9BLV9	09blv9 renilla mu
45	485.5	40.0	238	5	Q9BLV9	09blv9 renilla mu

ALIGNMENTS

RESULT 1

Q9U6Y8 PRELIMINARY; PRT; 225 AA.

```
AC Q9U6Y8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fluorescent protein PPS83.
OS Discosoma sp.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
OC Discosomatidae; Discosoma.
OX NCBI_Taxid=86600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9436614; PubMed=10504696;
RA Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
RA Markelov M.L., Lukyanov S.A.;
RT "Fluorescent proteins from nonbioluminescent Anthozoa species.";
RL Nat. Biotechnol. 17:969-973(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
RA Markelov M.L., Lukyanov S.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: ARI68419; AAF03369.1; -.
DR PDB: 1G7K; 07-NOV-01.
DR GO: GO:0006091; P:energy pathways; IEA.
DR InterPro: IPR009017; GFP like.
DR InterPro: IPR000786; Green_fl_protein.
DR Pfam: PF01353; GFP. 1.
DR PRINTS: PR01229; GFP. 1.
DR PRODOM: PD013756; Green_fl_protein. 1.
SQ SEQUENCE 225 AA; 25931 NM; FBF9A5369778F689 CRC64;
```

Query Match 100.0%; Score 1214; DB 5; Length 225;
Best local similarity 100.0%; Pred. No. 1.4e-101;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MRSSKNVFKEMRFKVRMEGVNGHEFEIEGEGSRPYEGHNTYKLTATKGGPLPFANDI 60
Db 1 MRSSKNVFKEMRFKVRMEGVNGHEFEIEGEGSRPYEGHNTYKLTATKGGPLPFANDI 60
Qy 61 LSPQGYSSKYVVKHPADIPDYKLSFPEGFKMERVMNFBEGVVTYVQDSSLQDGCFTY 120
Db 61 LSPQGYSSKYVVKHPADIPDYKLSFPEGFKMERVMNFBEGVVTYVQDSSLQDGCFTY 120
Qy 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Db 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Qy 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Db 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Qy 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTGRRHFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTGRRHFL 225

RESULT 2
Q9GTJ7 PRELIMINARY; PRT; 230 AA.
ID Q9GTJ7
AC Q9GTJ7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Red fluorescent protein.
GN
OS Discosoma sp. SSAL-2000.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
OC Discosomatidae; Discosoma.
OX NCBI_TaxID=137428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20434599; PubMed=10981720;
RA Fradkov A.F., Chen Y., Ding L., Barsova E.V., Matz M.V.,
RA Lukyanov S.A.;
RT "Novel fluorescent protein from Discosoma coral and its mutants
RT possesses a unique far-red fluorescence.";
RL FEBS Lett. 479:127-130(2000).
DR EMBL; AF272711; AAG16224.1; -.
DR HSSP; P42312; 1BFP.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PR01229; GFPLORESCENT.
DR ProDom; PD013756; Green fl protein; 1.
SQ SEQUENCE 230 AA; 26370 MW; 5215B1B436D7E51 CRC64;

Query Match 89.4%; Score 1085.5; DB 5; Length 230;
Best Local Similarity 88.1%; Pred. No. 5,8e-90;
Matches 199; Conservative 17; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MRSSKNVFKEMRFKVRMEGVNGHEFEIEGEGSRPYEGHNTYKLTATKGGPLPFANDI 60
Db 1 MRSSKNVFKEMRFKVRMEGVNGHEFEIEGEGSRPYEGHNTYKLTATKGGPLPFANDI 60
Qy 61 LSPQGYSSKYVVKHPADIPDYKLSFPEGFKMERVMNFBEGVVTYVQDSSLQDGCFTY 120
Db 61 LSPQGYSSKYVVKHPADIPDYKLSFPEGFKMERVMNFBEGVVTYVQDSSLQDGCFTY 120
Qy 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Db 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Qy 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Db 121 KVKFIGNVPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 180
Qy 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTGRRHFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTGRRHFL 225

RESULT 3
Q9SP04 PRELIMINARY; PRT; 221 AA.
ID Q9SP04
AC Q9SP04;

```

```

DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE GFP-like chromoprotein.
OS Goniodora tenuidens.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Fungina; Poritidae; Goniodora.
OX NCBI_TaxID=75301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21538626; PubMed=11682051;
RA Gurskaya N.G., Fradkov A.F., Tersikh A., Matz M.V., Labas Y.A.,
RA Martynov V.I., Yanshevich Y.G., Lukyanov K.A., Lukyanov S.A.;
RT "GFP-like chromoproteins as a source of far-red fluorescent
RT proteins(1).";
RL FEBS Lett. 507:16-20(2001).
DR EMBL; AF383156; AL27542.1; -.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green fl protein; 1.
SQ SEQUENCE 221 AA; 24918 MW; 93F9F4B5C2003CB4 CRC64;

Query Match 65.3%; Score 793; DB 5; Length 221;
Best Local Similarity 68.6%; Pred. No. 1,4e-63;
Matches 144; Conservative 25; Mismatches 41; Indels 0; Gaps 0;

Qy 6 NVIKEMRFKVRMEGVNGHEFEIEGEGSRPYEGHNTYKLTATKGGPLPFANDI 65
Db 2 SVIAKQMTYKVMSSGYVNGHYFVQDGGKRPYEGEYVTLVYTKGGPLPFANDI 61
Qy 66 QYGSKYVVKHPADIPDYKLSFPEGFKMERVMNFBEGVVTYVQDSSLQDGCFTY 125
Db 62 QYGSIPFTKYPEDIPDYKQSPFEGYTWERIMNFBEDAVCTVANDS1QGNCFYVVKFS 121
Qy 126 GVNFPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 185
Db 122 GVNFPSPDGPVMQKKTGMWEASTERYLPDGLVKGELHKALKLKDGGHYLVEPKSI 181
Qy 186 PVOLPGYYVDSKLDITSHNEDYTYVEQY 215
Db 182 PVKMPGYHYVDRKLDVTHNIDYTSVQCE 211

RESULT 4
Q9UGY7 PRELIMINARY; PRT; 232 AA.
ID Q9UGY7
AC Q9UGY7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fluorescent protein PA83.
OS Discosoma striata.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
OC Discosomatidae; Discosoma.
OX NCBI_TaxID=105400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436614; PubMed=10504696;
RA Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaitsev A.G.,
RA Markelov M.L., Lukyanov S.A.;
RT "Fluorescent proteins from nonbioluminescent Anthozoa species.";
RL Nat. Biotechnol. 17:969-973(1999).
DR EMBL; AF168420; AF03370.1; -.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PR01229; GFPLORESCENT.
DR ProDom; PD013756; Green fl protein; 1.
SQ SEQUENCE 232 AA; 26435 MW; AA8F18EE283CEAD CRC64;

```



```
Dh 2 SVIKPDMKIKLRMEGAVNGHNFVIEGEGKPKPEGTOTINLTVEGGLPFAVDILITNAF 61
Qy 66 QYGSKYVYKHPADIPDYKKLSPFEGFKWERVWNFEDGCVVTTQDSSLQ---DGCFTYKV 125
Dh 62 QYGNRAFTKYPRDIADYFKQSPFEGYSWERSMTYEDOGICITKSDIRMEGDCFTYKIRYD 121
Qy 126 GVNPPSDGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 185
Dh 122 GVNPPSDGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 181
Qy 186 FVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 223
Dh 182 RVQLPDYHFVDHRIEILSHDNDYNTVKLSENAEARYSM 219

RESULT 8
Q720W6 PRELIMINARY; PRT; 227 AA.
ID Q720W6
AC Q720W6.
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mc4;
RX MEDLINE=22689801; PubMed=12777529;
RA Kelmanon I.V., Matz M.V.;
RT "Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
RL Mol. Biol. Evol. 20:1125-1133(2003).
DR EMBL; AY181555; AAO61601.1; -
SQ SEQUENCE 227 AA; 2605 MW; 4BE2CB64FDB0E890 CRC64;

Query Match 56.0%; Score 679.5; DB 5; Length 227;
Best Local Similarity 54.3%; Pred. No. 2.6e-53;
Matches 120; Conservative 45; Mismatches 53; Indels 3; Gaps 1;

Qy 6 NVIKFPMFKYRMGTGNGHEFEIEGEGRPRYEGHNTVLTAKTKGGLPFAVDILITNAF 65
Dh 2 SVIKPDMKIKLRMEGAVNGHNFVIEGEGKPKPEGTOTINLTVEGGLPFAVDILITNAF 61
Qy 66 QYGSKYVYKHPADIPDYKKLSPFEGFKWERVWNFEDGCVVTTQDSSLQ---DGCFTYKV 122
Dh 62 DYGNRVFAKYPRDIADYFKQSPFEGYSWERSMTYEDOGICITATNDITMKGVDDCFYTKI 121
Qy 123 KFIGVNPSPDGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 182
Dh 122 RFDGVNFPANGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 181
Qy 183 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 223
Dh 182 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 222

RESULT 9
Q962P9 PRELIMINARY; PRT; 227 AA.
ID Q962P9
AC Q962P9.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea faveolata.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=48498;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RA Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
RA Falkowski P., Gorbunov M., Kolber Z.;
RT "Green Fluorescent Proteins in Caribbean Scleractinian Corals.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401282; AKK3923.1; -
DR GO; GO:0006091; P.energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR00786; Green_fl_protein.
DR Pfam; PF01353; GFP.1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;

Query Match 55.9%; Score 678.5; DB 5; Length 227;
Best Local Similarity 54.8%; Pred. No. 3.2e-53;
Matches 121; Conservative 44; Mismatches 53; Indels 3; Gaps 1;

Qy 6 NVIKFPMFKYRMGTGNGHEFEIEGEGRPRYEGHNTVLTAKTKGGLPFAVDILITNAF 65
Dh 2 SVIKPDMKIKLRMEGAVNGHNFVIEGEGKPKPEGTOTINLTVEGGLPFAVDILITNAF 61
Qy 66 QYGSKYVYKHPADIPDYKKLSPFEGFKWERVWNFEDGCVVTTQDSSLQ---DGCFTYKV 122
Dh 62 DYGNRVFAKYPRDIADYFKQSPFEGYSWERSMTYEDOGICVATNDITMKGVDDCFYTKI 121
Qy 123 KFIGVNPSPDGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 182
Dh 122 RFDGVNFPANGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 181
Qy 183 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 223
Dh 182 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 222

RESULT 10
Q720W8 PRELIMINARY; PRT; 227 AA.
ID Q720W8
AC Q720W8.
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mc2;
RX MEDLINE=22689801; PubMed=12777529;
RA Kelmanon I.V., Matz M.V.;
RT "Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
RL Mol. Biol. Evol. 20:1125-1133(2003).
DR EMBL; AY181553; AAO61599.1; -
SQ SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;

Query Match 55.9%; Score 678.5; DB 5; Length 227;
Best Local Similarity 54.8%; Pred. No. 3.2e-53;
Matches 121; Conservative 44; Mismatches 53; Indels 3; Gaps 1;

Qy 6 NVIKFPMFKYRMGTGNGHEFEIEGEGRPRYEGHNTVLTAKTKGGLPFAVDILITNAF 65
Dh 2 SVIKPDMKIKLRMEGAVNGHNFVIEGEGKPKPEGTOTINLTVEGGLPFAVDILITNAF 61
Qy 66 QYGSKYVYKHPADIPDYKKLSPFEGFKWERVWNFEDGCVVTTQDSSLQ---DGCFTYKV 122
Dh 62 DYGNRVFAKYPRDIADYFKQSPFEGYSWERSMTYEDOGICVATNDITMKGVDDCFYTKI 121
Qy 123 KFIGVNPSPDGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 182
Dh 122 RFDGVNFPANGPVWQKKTWMEASTERYLPDGVLTGGEIHAKLKDKGGHYLVEFKSIYMAKK 181
Qy 183 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 223
Dh 182 AKKPVOLPGYVYVDSKLDITSHNEDYTIYVEQYERTEGRHHL 222
```


DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fluorescent protein FP484.
OS Clavularia sp.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Alcyonacea;
OC Clavulariidae; Clavularia.
OX NCBI_TaxID=86521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9943614; PubMed=10504696;
RA Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Matkelev M.L., Lukyanov S.A.,
RT "Fluorescent proteins from nonbioluminescent Anthozoa species.",
RL Nat. Biotechnol. 17:969-973(1999).
DR EMBL/AF168424; AAF03374.1; -
DR GO:0006091; P:energy pathways; IEA.
DR InterPro: IPR009017; GFP_like.
DR InterPro: IPR00786; Green_fl_protein.
DR Pfam: PF01353; GFP; 1.
DR PRINTS: PR01229; GFPLORESCENT.
DR ProDom: PD013756; Green_fl_protein; 1.
SQ SEQUENCE 266 AA; 30450 MW; B4E97406E2708854 CRC64;

Query Match 54.9%; Score 667; DB 5; Length 266;
Best Local Similarity 54.8%; Pred. No. 4.3e-52;
Matches 121; Conservative 42; Mismatches 58; Indels 0; Gaps 0;

QY 3 SSKNVKEFMFKYMEGTGNGHEFEIEGEGRPYEGHNTVTLKVTKGPLPFAWDILS 62
DB 41 TTMGVIRKDMKIKLMEGNVNGHAFVIRGEGKPYDGTHTLNLVKEGAPLPFSYDILS 100
QY 63 PQFGSKVYVVKHPADIPDYKLSPEEGFKWERVWNFEDGVVTYTODSLQDGCFTYKV 122
DB 101 NAFQGNRALTKYPDIDADYFKQSPFEGYSWERTMTFEDKGIYKVSIDISMEEDSFIYEI 160
QY 123 KEIGVNPSPDGPVMOCKTMGWEASTERYPRDGVILKGIHKLKXKDGHYLVEFKSIYM 182
DB 161 RFDGNNFPNPGVPMOKTKLKEPSTELTYVRDGVILVGDISHSLLEGGGHYRCDFKSIYK 220
QY 183 AKKPVQLPGYVYVDSKLDITSHNEDYTYVEQYERTEGRHL 223
DB 221 AKKVVKLPDYHFDVDRIRIILNHDKDYNNKVTLYENAVARYSL 261

RESULT 15

Q8T6U0 PRELIMINARY; PRT; 236 AA.
AC Q8T6U0, 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Dendronephthya sp. SSAL-2002.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Alcyonaria; Alcyonacea;
OC Nephthidae; Dendronephthya.
OX NCBI_TaxID=191210;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21927629; PubMed=11929996;
RA Labas Y.A., Gurekaya N.G., Yamshevlch Y.G., Fradkov A.F.,
Lukyanov K.A., Lukyanov S.A., Matz M.V.,
RT "Diversity and evolution of the green fluorescent protein family.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:4256-4261(2002).
DR EMBL/AF420591; AAM10625.1; -
DR GO:0006091; P:energy pathways; IEA.
DR InterPro: IPR009017; GFP_like.
DR InterPro: IPR00786; Green_fl_protein.
DR Pfam: PF01353; GFP; 1.
DR PRINTS: PR01229; GFPLORESCENT.
DR ProDom: PD013756; Green_fl_protein; 1.
SQ SEQUENCE 236 AA; 26840 MW; CE1707CFF9334A90 CRC64;

Query Match 54.6%; Score 663; DB 5; Length 236;

Best Local Similarity 55.6%; Pred. No. 8.4e-52;
Matches 120; Conservative 38; Mismatches 58; Indels 0; Gaps 0;

QY 6 NVIKERFRFYRMEGTVNGHEFEIEGEGRPYEGHNTVTLKVTKGPLPFAWDILSPQF 65
DB 2 NLIKEDMRVYVNHGNGVNGHAFVIRGEGKPYEGQTLNLVKEGAPLPFSYDILTLAL 61
QY 66 QYSGKYVVKHPADIPDYKLSPEEGFKWERVWNFEDGVVTYTODSLQDGCFTYKVEI 125
DB 62 HYGNRVFTXEPADITDYFKQSPFEGYSWERTMTYEDKGICTIRSDISLEGDCFFQNIREF 121
QY 126 GUNFPSPDGPVMOCKTMGWEASTERYPRDGVILKGIHKLKXKDGHYLVEFKSIYMARK 185
DB 122 GNNFPNPGVPMOKTKLKEPSTELTHVRDGLLVGINLMALLLEGGGHYLCDFKTYKAKK 181
QY 186 PVQLPGYVYVDSKLDITSHNEDYTYVEQYERTEGRH 221
DB 182 VQULPDYHFDVDRIRIILSNDSDNKVTLYENGVARY 217

Search completed: July 8, 2004, 09:55:06
Job time: 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2004, 09:51:49 ; Search time 60 Seconds
(without alignments)
1059.553 Million cell updates/sec

Title: US-10-006-922a-12

Perfect score: 1214
Sequence: 1 MMSKRVIVKFMFKVMEG.....EDTIVEQYRTGRRHFL 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19808:*
2: geneseqp19808:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1214	100.0	225	3	AAI99836 Discosoma
2	1214	100.0	225	3	AAI99836 Discosoma
3	1214	100.0	225	4	AAI99836 Discosoma
4	1214	100.0	225	5	AAI99836 Discosoma
5	1214	100.0	225	5	AAI99836 Discosoma
6	1214	100.0	225	5	AAI99836 Discosoma
7	1214	100.0	225	5	AAI99836 Discosoma
8	1214	100.0	225	5	AAI99836 Discosoma
9	1214	100.0	225	5	AAI99836 Discosoma
10	1214	100.0	225	5	AAI99836 Discosoma
11	1214	100.0	225	5	AAI99836 Discosoma
12	1214	100.0	225	5	AAI99836 Discosoma
13	1214	100.0	225	5	AAI99836 Discosoma
14	1214	100.0	225	5	AAI99836 Discosoma
15	1214	100.0	225	5	AAI99836 Discosoma
16	1214	100.0	225	5	AAI99836 Discosoma
17	1214	100.0	225	5	AAI99836 Discosoma
18	1214	100.0	225	5	AAI99836 Discosoma
19	1214	100.0	225	5	AAI99836 Discosoma
20	1214	100.0	225	5	AAI99836 Discosoma
21	1214	100.0	225	5	AAI99836 Discosoma
22	1214	100.0	225	5	AAI99836 Discosoma
23	1214	100.0	225	5	AAI99836 Discosoma
24	1214	100.0	225	5	AAI99836 Discosoma
25	1214	100.0	225	5	AAI99836 Discosoma

26	1208	99.5	225	7	ABM00932	Abm00932 Discosoma
27	1208	99.5	225	7	ABM00935	Abm00935 Discosoma
28	1208	99.5	225	7	ABM00939	Abm00939 Discosoma
29	1207	99.4	225	5	AAE28921	AAE28921 Discosoma
30	1207	99.4	225	5	AAE28921	AAE28921 Discosoma
31	1207	99.4	225	7	ABM00941	Abm00941 Discosoma
32	1207	99.4	225	7	ABM00940	Abm00940 Discosoma
33	1206	99.3	225	7	ABM00933	Abm00933 Discosoma
34	1206	99.3	225	7	ABM00934	Abm00934 Discosoma
35	1205	99.3	240	6	ABP56678	ABP56678 Mammalian
36	1204	99.2	225	5	AAE28923	AAE28923 Discosoma
37	1204	99.2	225	5	AAE28925	AAE28925 Discosoma
38	1202	99.0	225	5	AAE28924	AAE28924 Discosoma
39	1202	99.0	240	6	ABP56685	ABP56685 Discosoma
40	1200	98.8	225	5	ABP70039	ABP70039 Colouir Fa
41	1199	98.8	225	5	AAE28926	AAE28926 Discosoma
42	1199	98.8	240	6	ABP56684	ABP56684 Discosoma
43	1199	98.8	240	6	ABP56683	ABP56683 Discosoma
44	1194	98.4	240	6	ABP56681	ABP56681 Discosoma
45	1193	98.3	240	6	ABP56679	ABP56679 Discosoma

ALIGNMENTS

RESULT 1	
AAI99836	standard; protein; 225 AA.
XX	
XX	AAI99836;
AC	
XX	
DT	12-SEP-2003 (revised)
DT	19-SEP-2000 (first entry)
XX	
DE	Discosoma sp. "red" novel fluorescent protein dFP583.
XX	
KW	Anthozoa; dFP583; fluorescent protein; non-bioluminescent organism;
KW	fluorescent labeling.
XX	
OS	Discosoma sp; "red".
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 122 /note= "encoded by TC"
FT	FT
FT	Misc-difference 127 /note= "encoded by GTTG"
XX	
PN	WO200034326-A1.
XX	
PD	15-JUN-2000.
XX	
PF	10-DEC-1999; 99WO-US029473.
XX	
PR	11-DEC-1998; 98US-00210330.
PR	14-OCT-1999; 99US-00418529.
XX	
PA	(CLON-) CLONTECH LAB INC.
XX	
PI	Lukyanov SA, Fradkov AF, Labas YA, Matz MV, Green G, Chen Y;
PI	Ding L;
DR	WPI; 2000-423381/36.
XX	
PT	Novel fluorescent protein from non-bioluminescent Discosoma sp. red,
PT	useful for fluorescent labeling and as markers.
PS	Claim 20; Page 74-75; 86pp; English.
XX	
CC	The present sequence is a novel fluorescent protein (nFP) encoded by the
CC	full-length cDNA dFP583. dFP583 was isolated from Discosoma sp. "red",
CC	a non-bioluminescent species of the Class Anthozoa. Fluorescent proteins
CC	can be used in fluorescent labeling, a useful tool for marking a protein,
CC	cell or organism of interest. Unlike other markers used in protein

CC labeling, such as beta-galactosidase and luciferase, fluorescent proteins
CC do not require an exogenous cofactor or substrate. Methods involving
CC fluorescent proteins are also less laborious and less difficult to
CC control than the traditional methods of fluorescent labeling, where a
CC protein of interest is purified and then covalently conjugated to a
CC fluorophore derivative. Novel fluorescent proteins isolated from species
CC of the Class Anthozoa can be used as markers for gene expression and
CC protein localization studies, and in fluorescence resonance energy
CC transfer (FRET) reactions. They may have improved properties and better
CC suitability for larger excitations compared to prior art fluorescent
CC proteins such as green fluorescent protein. (Updated on 12-SEP-2003 to
CC standardise OS field)

XX Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVIEKPMRPFVMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
DB 1 MRSSKNVIEKPMRPFVMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
QY 61 LSPQFGSKYVYKHPADIDPYKKLSFPEGFKMERVMNPFEDGGVVTYTQDSSLQDGCFTY 120
DB 61 LSPQFGSKYVYKHPADIDPYKKLSFPEGFKMERVMNPFEDGGVVTYTQDSSLQDGCFTY 120
QY 121 KYKFIGVNFPSDGPVMOKKTGMWEASTERYLPYRDGVLKGEIHKALKDKDGHYLVVERKSI 180
DB 121 KYKFIGVNFPSDGPVMOKKTGMWEASTERYLPYRDGVLKGEIHKALKDKDGHYLVVERKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 2

AAB01622 ID AAB01622 standard; protein; 225 AA.

XX AAB01622;

DT 12-DEC-2000 (first entry)

XX Discosoma sp. red fluorescent protein dFP583.

KW Anthozoa; fluorescent protein; fluorescence labeling; amFP486; cFP484;
KM zFP506; dFP538; dFP583; dFP483; asFP600; dFP512; dmFP592.

XX Discosoma sp.

OS Discosoma sp.

XX WO200034526-A1.

PD 15-JUN-2000.

PF 10-DEC-1999; 99WO-US029405.

PR 11-DEC-1998; 98US-00210330.

PA (CLON-) CLONTECH LAB INC.

PI Lukyanov SA, Fradkov AF, Labas YA, Matz MV;

DR WPI; 2000-423451/36.

PT Novel method for identifying a DNA sequence encoding fluorescent proteins
PT from non-bioluminescent Anthozoa which are useful for fluorescent
PT labeling and as markers.

PS Claim 3; Page 68-69; 73pp; English.

XX The present sequence is Discosoma sp. red fluorescent protein dFP583. It
CC was isolated using the Aequorea victoria green fluorescent protein (GFP)

CC sequence, which was used to design PCR primers which might isolate other
CC fluorescent proteins from a number of species of Anthozoa. These were
CC Anemonia majano, Clavularia sp., Zoanthus sp., Discosoma sp. and Anemonia
CC sulcata. The cDNA obtained was then screened in the search for sequences
CC encoding fluorescent proteins. The other proteins found in this manner
CC were cFP484, zFP506, dFP538, amFP486, dFP483, asFP600, dFP512 and
CC dmFP592. These proteins can be used as fluorescent labels (for gene
CC expression and protein localisation studies and in fluorescence resonance
CC energy transfer (FRET) studies) in place of fluorophore derivatives and
CC luciferases, as these involve laborious processes and the latter require
CC cofactors. They can also be used in place of GFP, which is too stable to
CC be useful when studying short-term or repetitive events

XX Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVIEKPMRPFVMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
DB 1 MRSSKNVIEKPMRPFVMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
QY 61 LSPQFGSKYVYKHPADIDPYKKLSFPEGFKMERVMNPFEDGGVVTYTQDSSLQDGCFTY 120
DB 61 LSPQFGSKYVYKHPADIDPYKKLSFPEGFKMERVMNPFEDGGVVTYTQDSSLQDGCFTY 120
QY 121 KYKFIGVNFPSDGPVMOKKTGMWEASTERYLPYRDGVLKGEIHKALKDKDGHYLVVERKSI 180
DB 121 KYKFIGVNFPSDGPVMOKKTGMWEASTERYLPYRDGVLKGEIHKALKDKDGHYLVVERKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 3

AAG65509 ID AAG65509 standard; protein; 225 AA.

XX AAG65509;

DT 30-NOV-2001 (first entry)

XX Anthozoan red fluorescent protein sequence.

DE Anthozoan red fluorescent protein; Anthozoan; fluorescence; marker; FRET; red.

XX Anthozoa.

OS Anthozoa.

XX WO200162919-A1.

PD 30-AUG-2001.

PF 13-FEB-2001; 2001WO-US004625.

PR 23-FEB-2000; 2000US-0184732P.

PA (AURO-) AURORA BIOSCIENCES CORP.

PI Nelson D, Zamaira E, Tsien R;

DR WPI; 2001-557704/62.

PT Proteins for fluorescence Resonance Energy Transfer (FRET) comprise
PT functional red fluorescent proteins, and the encoding nucleic acids, with
PT key mutations for improving the proteins function.

PS Disclosure; Page 85; 90pp; English.

XX The invention provides a nucleic acid encoding functional red fluorescent
CC protein (II) that differs from the sequence of an Anthozoan red
CC fluorescent protein by at least one amino acid substitution, and with

CC different fluorescent properties. The red fluorescent protein of the
CC invention can be expressed by standard recombinant methodology. (ii) are
CC used a fluorescent markers and FRET partners. It is used for identifying
CC protein-protein interactions. (ii) is also suitable for multiplexed
CC fluorescent analysis and FRET-based applications using existing Aquorea
CC fluorescent proteins. (ii) has improved brightness, reduced spectral
CC cross talk, and is rapidly and efficiently expressed in mammalian cells.
CC The key mutations in the encoding nucleic acids provide improved folding,
CC brightness, and create (ii) with sharper, more defined excitation and
CC emission peaks when expressed in mammalian cells. The present sequence
CC represents an anthozoan fluorescent protein

SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKVVIFKPMFKRMGTVNGHEFIEGEGRPYGHNTVKLKVTGGLPFAMDI 60
DB 1 MRSSKVVIFKPMFKRMGTVNGHEFIEGEGRPYGHNTVKLKVTGGLPFAMDI 60
QY 61 LSPQFOYGSKVYVYKHADIPDYKKLSFPEGFKMERVMNFEEDGVVTVTODSSLODGCFTY 120
DB 61 LSPQFOYGSKVYVYKHADIPDYKKLSFPEGFKMERVMNFEEDGVVTVTODSSLODGCFTY 120
QY 121 KYVFIVGNPPSDGPPVQOKKTMGWEASTERLYPRDGYLKGEIHKALKXDGHYLVEFKSI 180
DB 121 KYVFIVGNPPSDGPPVQOKKTMGWEASTERLYPRDGYLKGEIHKALKXDGHYLVEFKSI 180
QY 181 YMAKRPVOLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKRPVOLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

SeqIDNO:563drFP583

RESULT 4 ABB08834 standard; protein; 225 AA.

AC ABB08834;

DT 29-MAY-2002 (first entry)

DE Yeast optimised RFP SEQ ID NO 17.

KM Yeast: red fluorescent protein; RFP; plant; transgenic; GFP;

KM Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana;

KM Escherichia coli; green fluorescent protein; biotechnology.

OS Anthozoa.

PN DE20001395-U1.

PF 15-MAR-2001.

PR 27-JAN-2000; 2000DE-02001395.

PA (GPCR-) GPC BIOTECH AG.

DR WPI; 2002-228394/29.

DR N-PSDB; ABA95905, ABA95921, ABA95922.

PT New DNA encoding red fluorescent protein, useful as marker in

PT biotechnology, has sequence optimized for expression in eukaryotes,

PT especially yeast or plants.

PS Disclosure; Page 13-14; 19pp; German.

CC The invention relates to DNA (I) containing either sequence ABA95905 or

CC sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein

CC (YFP). (I) are used to express red fluorescent protein (RFP) in

CC eukaryotes, especially yeast, especially Saccharomyces cerevisiae and
CC plants, especially dicotyledonous plants including Nicotiana tabacum or
CC Arabidopsis thaliana and also in prokaryotes, especially bacteria,
CC especially Escherichia coli. RFP is useful in the same way as green
CC fluorescent protein but is more generally applicable in modern
CC biotechnology. (i) are optimised for expression in yeast and so generate
CC RFP at higher levels with stronger fluorescence and thus lowers the
CC detection limit and gives a better signal-to-noise ratio. The present
CC sequence is that of the yeast optimised RFP

SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKVVIFKPMFKRMGTVNGHEFIEGEGRPYGHNTVKLKVTGGLPFAMDI 60
DB 1 MRSSKVVIFKPMFKRMGTVNGHEFIEGEGRPYGHNTVKLKVTGGLPFAMDI 60
QY 61 LSPQFOYGSKVYVYKHADIPDYKKLSFPEGFKMERVMNFEEDGVVTVTODSSLODGCFTY 120
DB 61 LSPQFOYGSKVYVYKHADIPDYKKLSFPEGFKMERVMNFEEDGVVTVTODSSLODGCFTY 120
QY 121 KYVFIVGNPPSDGPPVQOKKTMGWEASTERLYPRDGYLKGEIHKALKXDGHYLVEFKSI 180
DB 121 KYVFIVGNPPSDGPPVQOKKTMGWEASTERLYPRDGYLKGEIHKALKXDGHYLVEFKSI 180
QY 181 YMAKRPVOLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKRPVOLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 5 AAE28833 standard; protein; 225 AA.

AC AAE28833;

DT 27-DEC-2002 (first entry)

DE Discosoma sp. drFP583 (NFP-6) wild-type protein.

KM Fluorescent protein; chromoprotein; protease cleavage assay; filter;

KM fluorescence activated cell sorting application; fluorescent timer;

KM biosensor; fluorescence resonance energy transfer application; FRET;

KM colouring agent; recombinant DNA application; analyte detection assay;

KM bioscreen; second messenger detector; drFP583 protein; NFP-6.

OS Discosoma sp.

PN WO200268459-A2.

PF 06-SEP-2002.

PR 20-FEB-2002; 2002WO-US005749.

PA 21-FEB-2001; 2001US-0270983P.

PR 04-DEC-2001; 2001US-00006922.

PA (CLON-) CLONTECH LAB INC.

DR Lukyanov S, Lukyanov K, Yanushevich Y, Savitsky A, Fradkov A;

DR WPI; 2002-691654/74.

DR N-PSDB; AAD46278.

PT New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant

PT of an aggregating Cnidarian chromo- or fluorescent protein or mutant for

PT analyte detection assays or fluorescence activated cell sorting

PS applications.

CC Disclosure; Page 70-71; 80pp; English.

```
XX The invention relates to nucleic acid molecules encoding non-aggregating
CC chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are
CC useful in analyte detection assays, as colouring agents, as markers in
CC recombinant DNA applications, as sunscreens or filters, in fluorescence
CC resonance energy transfer (FRET) applications, as biosensors in
CC prokaryotic and eukaryotic cells, in screening assays, as second
CC messenger detectors, in fluorescence activated cell sorting applications,
CC in protease cleavage assays or as fluorescent timers. The present
CC sequence is Discosoma sp. drfp583 (NFP-6) wild-type protein of the
CC invention
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEFMRFKVMRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
Db 1 MRSSKNVKEFMRFKVMRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
QY 61 LSPQFGSKVYVYKHPADIPDYKKLSFPEGFKMERVMNFDGGVYTVTQSSLDGCGFTY 120
Db 61 LSPQFGSKVYVYKHPADIPDYKKLSFPEGFKMERVMNFDGGVYTVTQSSLDGCGFTY 120
QY 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
Db 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
QY 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
Db 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225

RESULT 6
AAE17540
ID AAE17540 standard; protein; 225 AA.
XX
AC AAE17540;
XX
DT 22-APR-2002 (first entry)
XX
DE Discosoma sp. humanised wild-type Anthozoa protein drfp583.
XX
KW Fluorescent timer protein; protein movement; translocation; trafficking;
KW promoter activity; gene expression; transgenic plant; gene modification;
KW protein age; anthozoa protein; drfp583.
XX
OS Discosoma sp.
XX
XX WO200196373-A2.
XX
PN 20-DEC-2001.
XX
PD 13-JUN-2001; 2001WO-US019097.
XX
PF 14-JUN-2000; 2000US-0211607P.
XX
PR 14-JUN-2000; 2000US-0211607P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Fradkov AF, Terakikh A;
XX
PI WPI; 2002-154595/20.
XX
DR N-PSDB; AAD28207.
XX
PT New fluorescent timer proteins comprising an emission spectrum that
PT changes over time from a first wavelength to a second wavelength, useful
PT for monitoring intracellular protein movement, translocation, trafficking
PT or stability.
XX
PS Example 1; Fig 1; 89pp; English.
XX
```

```
CC The invention relates to a fluorescent timer protein having an emission
CC spectrum that changes over time after synthesis from a first wavelength
CC to a second wavelength. The fluorescent timer proteins are useful in
CC monitoring the activity of a promoter, determining the age of a protein,
CC identifying an agent that modulates the activity of a promoter and in
CC enriching a population of cells comprising a fluorescent timer protein.
CC The fluorescent timer proteins are also useful for assessing gene
CC expression during development of a multicellular organism or during
CC cellular differentiation, in response to a drug or other inducer of
CC promoter activity, as a reporter to serve as a read-out of promoter
CC activity, monitoring intracellular protein movement or translocation,
CC protein trafficking, or protein stability, to investigate temporal
CC aspects of the activity of a regulatory element, for determining cell
CC fate during development and organ remodeling, in spatial and temporal
CC visualisation of newly synthesised proteins and accumulated proteins, and
CC in distinguishing between newly formed and pre-existing structures, e.g.
CC membrane junctions and extracellular matrix components. The fluorescent
CC timer proteins may further be used to investigations where photobleaching
CC techniques are employed, as detectable labels, as selectable markers, as
CC biosensors in prokaryotic and eukaryotic cells, in protease cleavage
CC assays, and as second messenger detectors. The nucleic acids can be used
CC to generate transgenic, non-human plants or animals or site-specific gene
CC modifications in cell lines. The present sequence is Discosoma sp.
CC humanised wild-type Anthozoa protein drfp583 used for generating
CC fluorescent proteins
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEFMRFKVMRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
Db 1 MRSSKNVKEFMRFKVMRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTGKGPLPFAMD 60
QY 61 LSPQFGSKVYVYKHPADIPDYKKLSFPEGFKMERVMNFDGGVYTVTQSSLDGCGFTY 120
Db 61 LSPQFGSKVYVYKHPADIPDYKKLSFPEGFKMERVMNFDGGVYTVTQSSLDGCGFTY 120
QY 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
Db 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
QY 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
Db 121 KVKEFIGVNFPSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVVERKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225

RESULT 7
AAO18270
ID AAO18270 standard; protein; 225 AA.
XX
AC AAO18270;
XX
DT 26-SEP-2002 (first entry)
XX
DE Discosoma red fluorescent protein.
XX
KW Yeast; RAD54; promoter; genotoxicity cassette; cytotoxicity cassette;
KW modified yeast strain; environmental pollution.
XX
OS Discosoma sp.
XX
XX DE1061872-A1.
XX
PN 20-JUN-2002.
XX
PD 12-DEC-2000; 2000DB-01061872.
XX
PF 12-DEC-2000; 2000DB-01061872.
XX
PR 12-DEC-2000; 2000DB-01061872.
XX
PA (LICH/) LICHTENBERG-FRATTE H.
```

XX Lichtenberg-Frate H;
 PT WPI; 2002-539633/58.
 DR N-PSDB; AAL47952.
 XX Modified yeast strain, useful for detecting toxic compounds in
 PT environment, contains integrated cassettes responsive to genotoxic and
 PT cytotoxic compounds.
 XX
 PS Disclosure; Page 21-22; 34pp; German.
 XX
 CC The present invention relates to a modified yeast strain that contains,
 CC integrated stably and functionally in its genome, a genotoxicity cassette
 CC and a cytotoxicity cassette, each comprising a promoter and reporter
 CC gene, both of which are different in the two cassettes. The modified
 CC yeast strain is used to detect environmental pollution, especially
 CC genotoxic and/or cytotoxic substances in complex environmental
 CC contaminants, especially organic compounds, but also (non-)ionising
 CC radiation and chemical carcinogens. Particular applications are in
 CC monitoring (waste) water (e.g. as an early warning system), medical
 CC toxicology screening and for industrial process control. The present
 CC sequence is a marker protein suitable for use in the cassettes of the
 CC present invention
 CC
 XX Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 1214; DB 5; Length 225;
 Best Local Similarity 100.0%; Pred. No. 6.4e-128;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSKNVYKEFMKPKVMEGTGNGHEFEIEGEGRPYEGHNTVKLKVTGKGLPFPAMD 60
 Db 1 MRSSKNVYKEFMKPKVMEGTGNGHEFEIEGEGRPYEGHNTVKLKVTGKGLPFPAMD 60
 QY 61 LSPFOYGSKYVYKHADIPDYKLSFPEGFKMERVMNFEDEGVTYVTDSSLODGCFTY 120
 Db 61 LSPFOYGSKYVYKHADIPDYKLSFPEGFKMERVMNFEDEGVTYVTDSSLODGCFTY 120
 QY 121 KVFQIGVNFPSDGPVWQKTMGEASTERLYPRDGVYKGEIHKALKDKDGHYLVFKSI 180
 Db 121 KVFQIGVNFPSDGPVWQKTMGEASTERLYPRDGVYKGEIHKALKDKDGHYLVFKSI 180
 QY 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTVVEQYERTEGRHHLFL 225
 Db 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTVVEQYERTEGRHHLFL 225
 RESULT 8
 AAE34962 standard; protein; 225 AA.
 XX
 AC AAE34962;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Discosoma species red fluorescent protein (Rfp).
 XX
 KM phosphorylation indicator; fluorescent protein; detection; phosphatase;
 KM kinase; red fluorescent protein; Rfp.
 XX
 OS Discosoma sp.
 XX
 PN WO200295058-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 24-MAY-2002; 2002WO-US016955.
 XX
 PR 24-MAY-2001; 2001US-00865291.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX

PI Tsien RY, Ting AY, Zhang J;
 XX WPI; 2003-148474/14.
 DR N-PSDB; AAD53432.
 XX Novel chimeric phosphorylation indicators, useful for detecting
 PT kinase/phosphatase in samples, has donor molecule, phosphorylatable
 PT domain, phosphaminoacid binding domain, and acceptor molecule, in
 PT operative linkage.
 XX
 PS Disclosure; Col 65-66; 38pp; English.
 XX
 CC The present invention relates to chimeric phosphorylation indicators
 CC comprising a phosphorylation polypeptide and a fluorescent protein or in
 CC operative linkage, a donor molecule, a phosphorylatable domain, a
 CC phosphaminoacid binding domain (PABD) and an acceptor molecule. The
 CC phosphorylation indicators of the invention are useful for detecting
 CC kinases or phosphatases in a biological sample. They are also useful in
 CC high throughput analysis e.g. for detecting a kinase inhibitor or
 CC phosphatase inhibitor. The present sequence is Discosoma species red
 CC fluorescent protein (Rfp) used in the invention
 CC
 XX Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 1214; DB 6; Length 225;
 Best Local Similarity 100.0%; Pred. No. 6.4e-128;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSKNVYKEFMKPKVMEGTGNGHEFEIEGEGRPYEGHNTVKLKVTGKGLPFPAMD 60
 Db 1 MRSSKNVYKEFMKPKVMEGTGNGHEFEIEGEGRPYEGHNTVKLKVTGKGLPFPAMD 60
 QY 61 LSPFOYGSKYVYKHADIPDYKLSFPEGFKMERVMNFEDEGVTYVTDSSLODGCFTY 120
 Db 61 LSPFOYGSKYVYKHADIPDYKLSFPEGFKMERVMNFEDEGVTYVTDSSLODGCFTY 120
 QY 121 KVFQIGVNFPSDGPVWQKTMGEASTERLYPRDGVYKGEIHKALKDKDGHYLVFKSI 180
 Db 121 KVFQIGVNFPSDGPVWQKTMGEASTERLYPRDGVYKGEIHKALKDKDGHYLVFKSI 180
 QY 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTVVEQYERTEGRHHLFL 225
 Db 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTVVEQYERTEGRHHLFL 225
 RESULT 9
 ADC24126 standard; protein; 225 AA.
 XX
 AC ADC24126;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Discosoma wild-type red fluorescent protein.
 XX
 KM Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
 KM fluorescent protein variant; transcription induction detection;
 KM fluorescence energy resonance transfer; FRET; protein kinase;
 KM protein phosphatase; ion indicator.
 XX
 OS Discosoma.
 XX
 PN US2003059835-A1.
 XX
 PD 27-MAR-2003.
 XX
 PF 10-APR-2002; 2002US-00121258.
 XX
 PR 26-FEB-2001; 2001US-00794308.
 XX
 PR 24-MAY-2001; 2001US-00865538.
 XX
 PA (TSIE/) TSIE R Y.
 PA (CAMP/) CAMPBELL R E.

XX Tsien RY, Campbell RE;
P1 WPI; 2003-743764/70.
XX N-PSDB; ADOC24127, ADOC24134.
DR
XX
PT Novel polynucleotide sequence encoding Discosoma red fluorescent protein
PT variant having a reduced propensity to oligomerize, useful for detecting
PT transcriptional activity.
XX
PS Claim 1; SEQ ID NO 1; 67bp; English.
XX
CC The invention describes a polynucleotide sequence (I) encoding a
CC Discosoma red fluorescent protein (Dared) variant having a reduced
CC propensity to oligomerize, comprising amino acid substitutions at the AB
CC and/or AC interfaces of the wild-type Dared sequence (S1) comprising 225
CC amino acids, given in the specification, where the substitutions result
CC in reduced propensity of the Dared variant to form tetramers. (I) is
CC useful for detecting transcriptional activity by providing a host cell
CC containing a vector which comprises (I) operatively linked to an
CC expression control sequence, and an unit to assay the variant fluorescent
CC protein fluorescence, and assaying fluorescence of the variant
CC fluorescent protein produced by (VII), where variant fluorescent protein
CC fluorescence is indicative of transcriptional activity. A polynucleotide
CC encoding a fusion protein is useful for the analysis of in vivo
CC localisation or trafficking of a polypeptide of interest. A polypeptide
CC marker is useful as markers to identify the location and amount of a
CC target protein produced, where the target protein is fused to the marker,
CC as a complement to or alternative for the green fluorescent protein or
CC its spectral variant, for detecting induction of transcription, in
CC applications involving fluorescence energy resonance transfer (FRET),
CC which detects events as the function of the movement of fluorescent
CC donors and acceptors towards or away from each other, for making
CC fluorescent sensors for protein kinase and phosphatase activities or
CC indicators for ions and molecules such as Ca²⁺, Zn²⁺, for identifying the
CC presence of a molecule in a sample, for identifying a specific
CC interaction of a first and second molecule, for determining whether a
CC sample contains an enzyme or for determining the pH of the sample. (I) is
CC useful for identifying a region or condition that regulates the activity
CC of an expression control sequence. This is the amino acid sequence of
CC Discosoma wild-type red fluorescent protein.
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1214; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEPFMRFKVMEGTGNGHEFEIEGEGRGPRYEGHNTVTKLTGKGPLPFAMD 60
DB 1 MRSSKNVKEPFMRFKVMEGTGNGHEFEIEGEGRGPRYEGHNTVTKLTGKGPLPFAMD 60
QY 61 LSPQFGSKVYVYKHPADIDPYKKLSFPEGFKMERVWNFEDGAVVYTTQDSSLODGCFTY 120
DB 61 LSPQFGSKVYVYKHPADIDPYKKLSFPEGFKMERVWNFEDGAVVYTTQDSSLODGCFTY 120
QY 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
DB 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
QY 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
DB 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
DB 181 YMAKKPVQLPGYYVYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
RESULT 10
ID ABB00918 standard; protein; 225 AA.
XX ABB00918;
AC ABB00918;
XX
DT 15-JAN-2004 (first entry)
XX

DE Discosoma sp. red fluorescent protein (RFP).
XX
XX Fluorescent protein; resonance energy transfer; pH; detection;
KW red fluorescent protein; RFP.
XX
XX
OS Discosoma sp.
XX US2003170911-A1.
FN 11-SEP-2003.
XX
XX 26-FEB-2001; 2001US-00794308.
XX
XX 26-FEB-2001; 2001US-00794308.
XX
XX 26-FEB-2001; 2001US-00794308.
XX
PA (TSIE/) TSIE R Y.
PA (ZACH/) ZACHARIAS D A.
PA (BAIR/) BAIRD G S.
XX
P1 Tsien RY, Zacharias DA, Baird GS;
XX
XX WPI; 2003-802418/75.
DR N-PSDB; AAD61969.
XX
PT Fluorescent proteins containing a mutation that reduces or eliminates its
PT ability to oligomerize which gives more reliable fluorescence resonance
PT energy transfer results and are useful to detect molecule interaction,
PT enzymes, or sample pH.
XX
PS Claim 10; Page 30-31; Opp: English.
XX
CC The invention relates to a non-oligomerizing fluorescent protein
CC containing a mutation that reduces or eliminates its ability to
CC oligomerize. The fluorescent protein gives more reliable fluorescence
CC resonance energy transfer results and are useful to detect molecule
CC interaction, enzymes, or sample pH. These are also used to identify
CC agents or conditions that regulate expression of control sequences. The
CC present sequence is Discosoma sp. red fluorescent protein (RFP)
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1214; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 6,4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEPFMRFKVMEGTGNGHEFEIEGEGRGPRYEGHNTVTKLTGKGPLPFAMD 60
DB 1 MRSSKNVKEPFMRFKVMEGTGNGHEFEIEGEGRGPRYEGHNTVTKLTGKGPLPFAMD 60
QY 61 LSPQFGSKVYVYKHPADIDPYKKLSFPEGFKMERVWNFEDGAVVYTTQDSSLODGCFTY 120
DB 61 LSPQFGSKVYVYKHPADIDPYKKLSFPEGFKMERVWNFEDGAVVYTTQDSSLODGCFTY 120
QY 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
DB 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
QY 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
DB 121 KVFRTGVNPPSDGVPWQKKTGMWEASTERYLPYRPGVLTGSEIHKALKDKDGGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
DB 181 YMAKKPVQLPGYYVYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
RESULT 11
ID ABB08821 standard; protein; 487 AA.
XX ABB08821;
AC ABB08821;
XX
DT 28-MAY-2002 (first entry)
XX
DE Autofluorescent fusion protein A SEQ ID NO 1.
XX
KW Autofluorescent; fusion protein; proteolytic activity; fluorophore;

KM protease; assay; protease cleavage.
 XX Synthetic.
 OS
 XX WO200212543-A2.
 XX
 XX 14-FEB-2002.
 PD
 XX 07-AUG-2001; 2001WO-EP009112.
 XX PF
 XX 07-AUG-2000; 2000DE-01038382.
 XX PR
 XX (DIRE-) DIREVO BIOTECH AG.
 PA
 XX Kuhlmann R, Koltermann A, Ketting U, Schwille P;
 XX WPI; 2002-269094/31.
 DR
 XX
 XX New autofluorescent fusion protein, useful for determining protease and
 PT protease-inhibiting activity, comprises two different proteins linked by
 PT protease cleavage site.
 XX
 XX Example; Page 11; 35pp; German.
 PS
 XX The invention relates to an autofluorescing fusion protein (I, ABB08821-
 CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
 CC segment containing a protease cleavage site; and (iii) at least one
 CC different autofluorescing protein (Ib). Essentially no fluorescent energy
 CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
 CC quantifying protease (or protease-inhibitory) activity in liquid samples
 CC or cells, particularly for screening-based optimisation (or generation)
 CC of biomolecules with proteolytic activity. (I) can be prepared in
 CC cellular or cell-free systems and makes possible intracellular analysis
 CC of protease activity. Preparation of (I) does not require regioselective
 CC coupling of fluorophores to polypeptides and any selected protease
 CC cleavage site can be incorporated
 CC
 XX Sequence 487 AA:
 SQ
 Query Match 100.0%; Score 1214; DB 5; Length 487;
 Best Local Similarity 100.0%; Pred. No. 2e-127;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSKNVIEFMRPKYRMGEVTNGHEFEIEGEGRPYEGHNTVKKVTGKGLPFPAMD1 60
 DB 263 MRSSKNVIEFMRPKYRMGEVTNGHEFEIEGEGRPYEGHNTVKKVTGKGLPFPAMD1 322
 QY 61 LSPQFOYGSKVYVKHPADIPDYKLSFPEGFKMERVMNFDGCVVVTQDSSIQDGCFTY 120
 DB 323 LSPQFOYGSKVYVKHPADIPDYKLSFPEGFKMERVMNFDGCVVVTQDSSIQDGCFTY 382
 QY 121 KYVFIGVNFPSDGPVWQKKTWMEASTERLYPRDGVLKGEIHAKLKDGGHYLVEFKS1 180
 DB 383 KYVFIGVNFPSDGPVWQKKTWMEASTERLYPRDGVLKGEIHAKLKDGGHYLVEFKS1 442
 QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
 DB 443 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 487
 RESULT 12
 ABB08822
 ID ABB08822 standard; protein; 506 AA.
 XX
 AC ABB08822;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE Autofluorescent fusion protein B SEQ ID NO 2.
 XX
 KM Autofluorescent; fusion protein; proteolytic activity; fluorophore;
 KM protease; assay; protease cleavage.

OS Synthetic.
 XX
 XX WO200212543-A2.
 XX
 XX 14-FEB-2002.
 PD
 XX 07-AUG-2001; 2001WO-EP009112.
 XX PF
 XX 07-AUG-2000; 2000DE-01038382.
 XX PR
 XX (DIRE-) DIREVO BIOTECH AG.
 PA
 XX Kuhlmann R, Koltermann A, Ketting U, Schwille P;
 XX WPI; 2002-269094/31.
 DR
 XX
 XX New autofluorescent fusion protein, useful for determining protease and
 PT protease-inhibiting activity, comprises two different proteins linked by
 PT protease cleavage site.
 XX
 XX Claim 6; Page 11; 35pp; German.
 PS
 XX The invention relates to an autofluorescing fusion protein (I, ABB08821-
 CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
 CC segment containing a protease cleavage site; and (iii) at least one
 CC different autofluorescing protein (Ib). Essentially no fluorescent energy
 CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
 CC quantifying protease (or protease-inhibitory) activity in liquid samples
 CC or cells, particularly for screening-based optimisation (or generation)
 CC of biomolecules with proteolytic activity. (I) can be prepared in
 CC cellular or cell-free systems and makes possible intracellular analysis
 CC of protease activity. Preparation of (I) does not require regioselective
 CC coupling of fluorophores to polypeptides and any selected protease
 CC cleavage site can be incorporated
 CC
 XX Sequence 506 AA:
 SQ
 Query Match 100.0%; Score 1214; DB 5; Length 506;
 Best Local Similarity 100.0%; Pred. No. 2.1e-127;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSKNVIEFMRPKYRMGEVTNGHEFEIEGEGRPYEGHNTVKKVTGKGLPFPAMD1 60
 DB 282 MRSSKNVIEFMRPKYRMGEVTNGHEFEIEGEGRPYEGHNTVKKVTGKGLPFPAMD1 341
 QY 61 LSPQFOYGSKVYVKHPADIPDYKLSFPEGFKMERVMNFDGCVVVTQDSSIQDGCFTY 120
 DB 342 LSPQFOYGSKVYVKHPADIPDYKLSFPEGFKMERVMNFDGCVVVTQDSSIQDGCFTY 401
 QY 121 KYVFIGVNFPSDGPVWQKKTWMEASTERLYPRDGVLKGEIHAKLKDGGHYLVEFKS1 180
 DB 402 KYVFIGVNFPSDGPVWQKKTWMEASTERLYPRDGVLKGEIHAKLKDGGHYLVEFKS1 461
 QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 225
 DB 462 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRHHLFL 506
 RESULT 13
 ABB08823
 ID ABB08823 standard; protein; 547 AA.
 XX
 AC ABB08823;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE Autofluorescent fusion protein C SEQ ID NO 3.
 XX
 KM Autofluorescent; fusion protein; proteolytic activity; fluorophore;
 KM protease; assay; protease cleavage.
 OS Synthetic.

PN W0200212543-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-EP009112.
XX
PR 07-AUG-2000; 2000DE-01038382.
XX
PA (DIRE-) DIREVO BIOTECH AG.
XX
PI Kuhlmann R, Koltermann A, Ketting U, Schwille P;
XX WPI; 2002-269094/31.
XX
DR New autofluorescent fusion protein, useful for determining protease and
XX protease-inhibiting activity, comprises two different proteins linked by
XX protease cleavage site.
XX
PS Claim 6; Page 11; 35pp; German.
XX
CC The invention relates to an autofluorescing fusion protein (I), ABB08821-
CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
CC segment containing a protease cleavage site; and (iii) at least one
CC different autofluorescing protein (Ib). Essentially no fluorescent energy
CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
CC quantifying protease (or protease-inhibitory) activity in liquid samples
CC or cells, particularly for screening-based optimization (or generation)
CC of biomolecules with proteolytic activity. (I) can be prepared in
CC cellular or cell-free systems and makes possible intracellular analysis
CC of protease activity. Preparation of (I) does not require regioselective
CC coupling of fluorophores to polypeptides and any selected protease
CC cleavage site can be incorporated
CC
SQ Sequence 547 AA;
XX
Query Match 100.0%; Score 1214; DB 5; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MRSSKNVYKEFMRFKVMETGVNGHEFEIEBEGEGRPYEGHNTVYKLTGKGPPLPFAWDI 60
DB 323 MRSSKNVYKEFMRFKVMETGVNGHEFEIEBEGEGRPYEGHNTVYKLTGKGPPLPFAWDI 382
XX
QY 61 LSPQFGSKYVYVHPADIPDYKLSPEEGFKMERVWNPFDGGVVTYTDSSLDGCFIY 120
DB 383 LSPQFGSKYVYVHPADIPDYKLSPEEGFKMERVWNPFDGGVVTYTDSSLDGCFIY 442
XX
QY 121 KVFYGVNPPSDGVPWQKKTGWGEASTERLYPRDGLVKGSIHKLKLDGSHYLVFEXSI 180
DB 443 KVFYGVNPPSDGVPWQKKTGWGEASTERLYPRDGLVKGSIHKLKLDGSHYLVFEXSI 502
XX
QY 181 YMAKKPVQLPGYYVVDKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 503 YMAKKPVQLPGYYVVDKLDITSHNEDYTIIVEQYERTEGRHHLFL 547
XX
RESULT 14
AAE28920
ID AAE28920 standard; protein; 225 AA.
XX
AC AAE28920;
XX
DT 27-DEC-2002 (first entry)
XX
DE Diacosoma sp. drfp583 (NFP-6) mutant protein, E5 (S197T).
XX
KM Fluorescent protein; chromoprotein; protease cleavage assay; filter;
KM fluorescence activated cell sorting application; fluorescent timer;
KM biosensor; fluorescence resonance energy transfer application; FRET;
KM colouring agent; recombinant DNA application; analyte detection assay;
KM sunscreen; second messenger detector; drfp583 protein; NFP-6; mutant;
KM mutcin.
XX

OS Diacosoma sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
XX Misc-difference 197
FT /note="Wild-type Ser substituted with Thr"
XX
XX W0200268459-A2.
XX
XX 06-SEP-2002.
XX
XX 20-FEB-2002; 2002WO-US005749.
XX
XX 21-FEB-2001; 2001US-0270983P.
XX 04-DEC-2001; 2001US-00006922.
XX
XX (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov S, Lukyanov K, Yanushevich Y, Savitsky A, Fradkov A;
XX WPI; 2002-691654/74.
XX
DR New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant
XX of an aggregating Cnidarian chromo- or fluorescent protein or mutant for
XX analyte detection assays or fluorescence activated cell sorting
XX applications.
XX
PS Disclosure; Page; 80pp; English.
XX
CC The invention relates to nucleic acid molecules encoding non-aggregating
CC chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are
CC useful in analyte detection assays, as colouring agents, as markers in
CC recombinant DNA applications, as sunscreens or filters, in fluorescence
CC resonance energy transfer (FRET) applications, as biosensors in
CC prokaryotic and eukaryotic cells, in screening assays, as second
CC messenger detectors, in fluorescence activated cell sorting applications,
CC in protease cleavage assays or as fluorescent timers. The present
CC sequence is Diacosoma sp. drfp583 (NFP-6) mutant protein of the
CC invention. Note: This sequence is not shown in the specification, but is
CC derived from Diacosoma sp. drfp583 (NFP-6) wild-type protein shown as SEQ
XX ID NO:8 (AAE28833) in page 70-71 of the specification
XX
SQ Sequence 225 AA;
XX
Query Match 99.8%; Score 1211; DB 5; Length 225;
Best Local Similarity 99.6%; Pred. No. 1.4e-127;
Matches 224; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MRSSKNVYKEFMRFKVMETGVNGHEFEIEBEGEGRPYEGHNTVYKLTGKGPPLPFAWDI 60
DB 1 MRSSKNVYKEFMRFKVMETGVNGHEFEIEBEGEGRPYEGHNTVYKLTGKGPPLPFAWDI 60
XX
QY 61 LSPQFGSKYVYVHPADIPDYKLSPEEGFKMERVWNPFDGGVVTYTDSSLDGCFIY 120
DB 61 LSPQFGSKYVYVHPADIPDYKLSPEEGFKMERVWNPFDGGVVTYTDSSLDGCFIY 120
XX
QY 121 KVFYGVNPPSDGVPWQKKTGWGEASTERLYPRDGLVKGSIHKLKLDGSHYLVFEXSI 180
DB 121 KVFYGVNPPSDGVPWQKKTGWGEASTERLYPRDGLVKGSIHKLKLDGSHYLVFEXSI 180
XX
QY 181 YMAKKPVQLPGYYVVDKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVVDKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
XX
RESULT 15
ABW00937
ID ABW00937 standard; protein; 225 AA.
XX
AC ABW00937;
XX
DT 15-JAN-2004 (first entry)
XX

DE Discosoma sp. red fluorescent protein (RFP), S197T.
 XX Fluorescent protein; resonance energy transfer; pH; detection;
 KW red fluorescent protein; RFP; mutant; mutein.
 XX
 XX Discosoma sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 197 /note= "Wild-type Ser is substituted with Thr"
 FT
 XX
 XX US2003170911-A1.
 PN
 XX
 XX 11-SEP-2003.
 PD
 XX 26-FEB-2001; 2001US-00794308.
 XX
 XX 26-FEB-2001; 2001US-00794308.
 XX
 XX (TSIE/) TSIE R Y.
 XX (ZACH/) ZACHARIAS D A.
 XX (BAIR/) BAIRD G S.
 XX
 PI Tsien RY, Zacharias DA, Baird GS;
 XX
 XX WPI; 2003-802418/75.
 XX
 XX Fluorescent proteins containing a mutation that reduces or eliminates its
 PT ability to oligomerize which gives more reliable fluorescence resonance
 PT energy transfer results and are useful to detect molecule interaction,
 PT enzymes, or sample pH.
 XX
 XX Example 2; Page; Opp; English.
 PS
 XX The invention relates to a non-oligomerising fluorescent protein
 CC containing a mutation that reduces or eliminates its ability to
 CC oligomerise. The fluorescent protein gives more reliable fluorescence
 CC resonance energy transfer results and are useful to detect molecule
 CC interaction, enzymes, or sample pH. These are also used to identify
 CC agents or conditions that regulate expression of control sequences. The
 CC present sequence is Discosoma sp. red fluorescent protein (RFP) mutant.
 CC Note: This sequence is not shown in the specification, however this
 CC sequence is constructed based on Discosoma sp. wild-type RFP protein
 CC shown in page 30-31 (ABW00918)
 XX
 XX
 SQ Sequence 225 AA:
 Query Match 99.8%; Score 1211; DB 7; Length 225;
 Best Local Similarity 99.6%; Pred. No. 1,4e-127;
 Matches 224; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSKNVYKEFMFKRMETVNGHEPFIKSGEGRPYEGHNTVKLKVTGSGPLPFAWDI 60
 DB 1 MRSSKNVYKEFMFKRMETVNGHEPFIKSGEGRPYEGHNTVKLKVTGSGPLPFAWDI 60
 QY 61 LSPQFYGSKVYVYKHPADIPDYKKLSFPEGFKWERVWVNFEDGGVVTYTDSSLDGCFIY 120
 DB 61 LSPQFYGSKVYVYKHPADIPDYKKLSFPEGFKWERVWVNFEDGGVVTYTDSSLDGCFIY 120
 QY 121 KVFPIGVNFPSPDGPVWQKTMGEASTERLYPRDGVKGIHAKLKDGGHYLVEFKSI 180
 DB 121 KVFPIGVNFPSPDGPVWQKTMGEASTERLYPRDGVKGIHAKLKDGGHYLVEFKSI 180
 QY 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTIIVEOYERTEGRHHLFL 225
 DB 181 YMAKKPVQLPGYVYVDSKLDITSHNEDYTIIVEOYERTEGRHHLFL 225

Search completed: July 8, 2004, 09:53:04
 Job time : 61 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 08:23:25 ; Search time 2083 Seconds

(without alignments)
14107.814 Million cell updates/sec

Title: US-10-006-922A-11

Perfect score: 678
Sequence: 1 atgaagctctccaagaatgt.....gccaccatctgtcctttaa 678

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vtl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	6 AR183915	AR183915 Sequence
2	678	100.0	678	6 AX172854	AX172854 Sequence
3	678	100.0	678	6 AX207715	AX207715 Sequence
4	678	100.0	678	6 AX233581	AX233581 Sequence
5	678	100.0	859	3 AF168419	AF168419 Discomoma
6	678	100.0	859	6 AX463698	AX463698 Sequence
7	665	98.1	666	6 AX348043	AX348043 Sequence
8	665	98.1	666	6 AX353910	AX353910 Sequence
9	658.8	97.2	666	6 AX686888	AX686888 Sequence
10	566.4	83.5	876	3 AF272711	AF272711 Discomoma
11	566.4	83.5	876	6 AX686884	AX686884 Sequence
12	449.8	66.3	681	6 AX233584	AX233584 Sequence
13	449.8	66.3	713	6 AX233627	AX233627 Sequence
14	449.2	66.3	678	6 AX370404	AX370404 Sequence
15	449.2	66.3	678	6 AX824725	AX824725 Sequence
16	447.2	66.0	4592	6 AX463702	AX463702 Sequence
17	447.2	66.0	9320	6 AX663075	AX663075 Sequence
18	446	65.8	678	6 AX370406	AX370406 Sequence
19	445.8	65.8	6893	6 AX823860	AX823860 Sequence
20	439.6	64.8	678	6 AX370408	AX370408 Sequence
21	438	64.6	678	6 AX824732	AX824732 Sequence
22	437	64.5	1050	6 AX666133	AX666133 Sequence
23	435.6	64.2	675	6 AX824731	AX824731 Sequence
24	434.6	64.1	850	6 AX686886	AX686886 Sequence
25	432.2	63.7	1041	12 AY342347	AY342347 Red H-Pel
26	432.2	63.7	10276	12 AY423448	AY423448 Red H-Sti
27	410.2	60.5	681	12 AF506025	AF506025 Synthetic
28	410.2	60.5	1395	12 AF506026	AF506026 Synthetic
29	409.6	60.4	699	6 AR183914	AR183914 Sequence
30	409.6	60.4	699	6 AX172853	AX172853 Sequence
31	409.6	60.4	699	6 AX207714	AX207714 Sequence
32	409.6	60.4	699	6 AX233580	AX233580 Sequence
33	409.6	60.4	960	3 AF168420	AF168420 Discomoma
34	404	59.6	404	6 AX815529	AX815529 Sequence
35	396	58.4	881	3 AF383156	AF383156 Gonipora
36	393.2	58.0	660	6 AX699771	AX699771 Sequence
37	393.2	58.0	660	6 AX699773	AX699773 Sequence
38	393.2	58.0	660	6 AX699777	AX699777 Sequence
39	393.2	58.0	660	6 AX699803	AX699803 Sequence
40	393.2	58.0	660	6 AX699805	AX699805 Sequence
41	393.2	58.0	660	6 AX699815	AX699815 Sequence
42	393.2	58.0	660	6 AX699817	AX699817 Sequence
43	393.2	58.0	678	6 AX824729	AX824729 Sequence
44	391.6	57.8	660	6 AX699779	AX699779 Sequence
45	391.6	57.8	660	6 AX699813	AX699813 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR183915 678 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6342379.
ACCESSION AR183915
VERSION AR183915.1 GI:20227884
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 678)
AUTHORS Teien,R.Y. and Gonzalez,J.R. III.
TITLE Detection of transmembrane potentials by optical methods
JOURNAL Patent: US 6342379-A 6 29-JUN-2002;
FEATURES Location/Qualifiers

source 1. .678
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTTCCCAAGATGTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGCTTCCCAAGATGTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACGGTCAATGGGCAAGATTGAAATAGAGGCGAAGGAGGAGGCGCATACGAAGGC 120
DB 61 ACGGTCAATGGGCAAGATTGAAATAGAGGCGAAGGAGGAGGCGCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGCTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGCTGGGATTT 180
QY 181 TTGTACACCAATTTCAATATGAAAGCAAGGATATATGCAAGCACTTCCGATACCA 240
DB 181 TTGTACACCAATTTCAATATGAAAGCAAGGATATATGCAAGCACTTCCGATACCA 240
QY 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGTCATGAATTGAA 300
DB 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGTCATGAATTGAA 300
QY 301 GACGTTGGCGTCTGTACTGTAAACCAAGGATTCAGATTGCAAGATGGCTGTTCATCTAC 360
DB 301 GACGTTGGCGTCTGTACTGTAAACCAAGGATTCAGATTGCAAGATGGCTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATTTGGCGTGAATCTTCCGATGAGCCTGTTATGCAAAAGAGCA 420
DB 361 AAGGTCAAGTTCAATTTGGCGTGAATCTTCCGATGAGCCTGTTATGCAAAAGAGCA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGCGGTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGCGGTGTTGAAAGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGTTGGTCACTCTAGTTGAATCAAAAGTAT 540
DB 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGTTGGTCACTCTAGTTGAATCAAAAGTAT 540
QY 541 TACATGGAAGAAAGCCTGTGAGCTACCAAGGTTCTATGTTGACTCCAAACTGAT 600
DB 541 TACATGGAAGAAAGCCTGTGAGCTACCAAGGTTCTATGTTGACTCCAAACTGAT 600
QY 601 ATTAACAAGCCACACGAAGACTATACATGTTGAGCGTATGAAAGAACGAGGAGCGC 660
DB 601 ATTAACAAGCCACACGAAGACTATACATGTTGAGCGTATGAAAGAACGAGGAGCGC 660
QY 661 CACCATCTGTTCCCTTTAA 678
DB 661 CACCATCTGTTCCCTTTAA 678

RESULT 2
AX172854 678 bp DNA linear PAT 03-JUL-2001
LOCUS
DEFINITION Sequence 6 from Patent WO0142211.
ACCESSION AX172854
VERSION AX172854.1 GI:14597903
KEYWORDS
SOURCE
ORGANISM
Discosoma sp.
Eukaryota; Metazoa; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discosoma.

REFERENCE
AUTHORS Tsien, R.Y. and Gonzalez, J.E.
TITLE Detection of transmembrane potentials by optical methods
JOURNAL Patent: WO 0142211-A 6 14-JUN-2001;

FEATURES
source The Regents of the University of California (US)
1. .678
/organism="Discosoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"

ORIGIN

Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTTCCCAAGATGTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGCTTCCCAAGATGTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACGGTCAATGGGCAAGATTGAAATAGAGGCGAAGGAGGAGGCGCATACGAAGGC 120
DB 61 ACGGTCAATGGGCAAGATTGAAATAGAGGCGAAGGAGGAGGCGCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGCTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGCTGGGATTT 180
QY 181 TTGTACACCAATTTCAATATGAAAGCAAGGATATATGCAAGCACTTCCGATACCA 240
DB 181 TTGTACACCAATTTCAATATGAAAGCAAGGATATATGCAAGCACTTCCGATACCA 240
QY 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGTCATGAATTGAA 300
DB 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGTCATGAATTGAA 300
QY 301 GACGTTGGCGTCTGTACTGTAAACCAAGGATTCAGATTGCAAGATGGCTGTTCATCTAC 360
DB 301 GACGTTGGCGTCTGTACTGTAAACCAAGGATTCAGATTGCAAGATGGCTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATTTGGCGTGAATCTTCCGATGAGCCTGTTATGCAAAAGAGCA 420
DB 361 AAGGTCAAGTTCAATTTGGCGTGAATCTTCCGATGAGCCTGTTATGCAAAAGAGCA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGCGGTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGCGGTGTTGAAAGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGTTGGTCACTCTAGTTGAATCAAAAGTAT 540
DB 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGTTGGTCACTCTAGTTGAATCAAAAGTAT 540
QY 541 TACATGGAAGAAAGCCTGTGAGCTACCAAGGTTCTATGTTGACTCCAAACTGAT 600
DB 541 TACATGGAAGAAAGCCTGTGAGCTACCAAGGTTCTATGTTGACTCCAAACTGAT 600
QY 601 ATTAACAAGCCACACGAAGACTATACATGTTGAGCGTATGAAAGAACGAGGAGCGC 660
DB 601 ATTAACAAGCCACACGAAGACTATACATGTTGAGCGTATGAAAGAACGAGGAGCGC 660
QY 661 CACCATCTGTTCCCTTTAA 678
DB 661 CACCATCTGTTCCCTTTAA 678

RESULT 3
AX207715 678 bp DNA linear PAT 31-AUG-2001
LOCUS
DEFINITION Sequence 13 from Patent WO0157242.
ACCESSION AX207715
VERSION AX207715.1 GI:15422399
KEYWORDS
SOURCE
ORGANISM
Discosoma sp.
Eukaryota; Metazoa; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discosoma.

REFERENCE
1

AUTHORS Stack,J.H., Whitney,M., Cubitt,A.B. and Pollok,B.A.
TITLE Methods of protein destabilization and uses thereof
JOURNAL Patent: WO 0157242-A 13 09-AUG-2001;
Aurora Biosciences Corporation (US)
FEATURES
source 1..678
/organism="Discosoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"
ORIGIN
Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAGTTCCGATGAAAGA 60
Db 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAGTTCCGATGAAAGA 60
Qy 61 ACGGTCAATGGGACGAGTTTGAATGAAGCGAAGAGAGGAGGCGCATACGAAGGC 120
Db 61 ACGGTCAATGGGACGAGTTTGAATGAAGCGAAGAGAGGAGGCGCATACGAAGGC 120
Qy 121 CACAATACCGTTAAAGCTTAAGTTAACCAAGGGGGACCTTGGCATTGGTGGATATT 180
Db 121 CACAATACCGTTAAAGCTTAAGTTAACCAAGGGGGACCTTGGCATTGGTGGATATT 180
Qy 181 TTGTCAACAATTTCAATGAGTGAAGCAAGTATATGTCAGACCCCTCGACATACCA 240
Db 181 TTGTCAACAATTTCAATGAGTGAAGCAAGTATATGTCAGACCCCTCGACATACCA 240
Qy 241 GACTATATAAAGCTGTCATTCTGAAAGATTAAATGGAAGAGGTCAATGAACCTTTGAA 300
Db 241 GACTATATAAAGCTGTCATTCTGAAAGATTAAATGGAAGAGGTCAATGAACCTTTGAA 300
Qy 301 GACGTCGCGCTGTTACTGTAAACCCAGATTCAGATTGCAAGATGGCTGTTTCACTAC 360
Db 301 GACGTCGCGCTGTTACTGTAAACCCAGATTCAGATTGCAAGATGGCTGTTTCACTAC 360
Qy 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGACCTGTTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGACCTGTTATGCAAAAGAGACA 420
Qy 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGATGAGCGTGTGAAAGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGATGAGCGTGTGAAAGAGAG 480
Qy 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTGTCTATTACTAGTTGAATTCAAAAGTATT 540
Db 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTGTCTATTACTAGTTGAATTCAAAAGTATT 540
Qy 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTAGTTGATCTCAAACTGGAT 600
Db 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTAGTTGATCTCAAACTGGAT 600
Qy 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAGAACCGAGGAGCGC 660
Db 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAGAACCGAGGAGCGC 660
Qy 661 CACCATCTGTTCTTTAA 678
Db 661 CACCATCTGTTCTTTAA 678
RESULT 4
AX233581 678 bp DNA linear PAT 11-SEP-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0162919.
ACCESSION AX233581
VERSION AX233581.1 GI:15593305
KEYWORDS
SOURCE Discosoma sp.
ORGANISM Discosoma sp.

REFERENCE
AUTHORS Nelson,D., Zamaire,E. and Tsien,R.
TITLE Modified fluorescent proteins
JOURNAL Patent: WO 0162919-A 5 30-AUG-2001;
Aurora Biosciences Corporation (US)
FEATURES
source 1..678
/organism="Discosoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"
/note="red"
ORIGIN
Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAGTTCCGATGAAAGA 60
Db 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAGTTCCGATGAAAGA 60
Qy 61 ACGGTCAATGGGACGAGTTTGAATGAAGCGAAGAGAGGAGGCGCATACGAAGGC 120
Db 61 ACGGTCAATGGGACGAGTTTGAATGAAGCGAAGAGAGGAGGCGCATACGAAGGC 120
Qy 121 CACAATACCGTTAAAGCTTAAGTTAACCAAGGGGGACCTTGGCATTGGTGGATATT 180
Db 121 CACAATACCGTTAAAGCTTAAGTTAACCAAGGGGGACCTTGGCATTGGTGGATATT 180
Qy 181 TTGTCAACAATTTCAATGAGTGAAGCAAGTATATGTCAGACCCCTCGACATACCA 240
Db 181 TTGTCAACAATTTCAATGAGTGAAGCAAGTATATGTCAGACCCCTCGACATACCA 240
Qy 241 GACTATATAAAGCTGTCATTCTGAAAGATTAAATGGAAGAGGTCAATGAACCTTTGAA 300
Db 241 GACTATATAAAGCTGTCATTCTGAAAGATTAAATGGAAGAGGTCAATGAACCTTTGAA 300
Qy 301 GACGTCGCGCTGTTACTGTAAACCCAGATTCAGATTGCAAGATGGCTGTTTCACTAC 360
Db 301 GACGTCGCGCTGTTACTGTAAACCCAGATTCAGATTGCAAGATGGCTGTTTCACTAC 360
Qy 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGACCTGTTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGACCTGTTATGCAAAAGAGACA 420
Qy 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGATGAGCGTGTGAAAGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGATGAGCGTGTGAAAGAGAG 480
Qy 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTGTCTATTACTAGTTGAATTCAAAAGTATT 540
Db 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTGTCTATTACTAGTTGAATTCAAAAGTATT 540
Qy 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTAGTTGATCTCAAACTGGAT 600
Db 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTAGTTGATCTCAAACTGGAT 600
Qy 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAGAACCGAGGAGCGC 660
Db 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAGAACCGAGGAGCGC 660
Qy 661 CACCATCTGTTCTTTAA 678
Db 661 CACCATCTGTTCTTTAA 678
RESULT 5
AF168419 859 bp mRNA linear INV 27-JUL-2001
LOCUS
DEFINITION Discosoma sp. fluorescent protein FP583 mRNA, complete cds.
ACCESSION AF168419

VERSION AF168419.2 GI:7105733
KEYWORDS
SOURCE Discosoma sp.
ORGANISM Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia; Discosomatidae; Discosoma.
REFERENCE
AUTHORS 1 (bases 1 to 859)
Matz, M.V., Fradkov, A.F., Labas, Y.A., Savitsky, A.P., Zaraisky, A.G.,
Markelov, M.L. and Lukyanov, S.A.
TITLE Fluorescent proteins from nonbioluminescent Anthozoa species
JOURNAL Nat. Biotechnol. 17 (10), 969-973 (1999)
MEDLINE 99436614
PIRBASE 10504686
REFERENCE 2 (bases 1 to 859)
Matz, M.V., Fradkov, A.F., Labas, Y.A., Savitsky, A.P., Zaraisky, A.G.,
Markelov, M.L. and Lukyanov, S.A.
AUTHORS Direct Submission
TITLE Submitted (14-JUL-1999) Institute of Bioorganic Chemistry RAS,
JOURNAL Mikhukho-Maklaya 16/10, Moscow 117871, Russia
REFERENCE 3 (bases 1 to 859)
Matz, M.V., Fradkov, A.F., Labas, Y.A., Savitsky, A.P., Zaraisky, A.G.,
Markelov, M.L. and Lukyanov, S.A.
AUTHORS Direct Submission
TITLE Submitted (25-FEB-2000) Institute of Bioorganic Chemistry RAS,
JOURNAL Mikhukho-Maklaya 16/10, Moscow 117871, Russia
REMARK Sequence update by submitter
COMMENT On Feb 25, 2000 this sequence version replaced gi:6090866.
FEATURES
SOURCE 1..859
/organism="Discosoma sp."
/mol_type="mRNA"
/db_xref="taxon:86600"
54..731
/note="GFP-like protein; orange-red"
/codon_start=1
/product="fluorescent protein FP583"
/protein_id="AAF03369.1"
/db_xref="GI:6090867"
/translation="MRSKNVLEKEMRPFVMEGTVNGHEFEIEGEGRPYEGHNTV
KLKVTGGPILPFAWDILSPQYGSKYVYKHADIPDYKLSPEGFKEWVNFEDG
GVATVTDSSLDQGCFTYKVFIGNPDSQVPMQKTKGMEASTERYLPDQVLGE
IHKALKIKDGGHYLVEFKSIYMAKKPQVLPGYVYVDSKLDITSHNEDYTIIVEQYERIE
GRHHLFL"
ORIGIN
Query Match 100.0%; Score 678; DB 3; Length 859;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGATTGATGAGTTTAAAGTTGCGATGGAAGA 60
DB 54 ATGAGGCTTCCAGAAATGTTATCAAGAGATTGATGAGTTTAAAGTTGCGATGGAAGA 113
QY 61 ACGGTCATGGGCGACGATTTGAAATAGAAAGCCAGAGAGGAGGAGCCATAGGAAGC 120
DB 114 ACGGTCATGGGCGACGATTTGAAATAGAAAGCCAGAGAGGAGGAGCCATAGGAAGC 173
QY 121 CACATACCGTAAAGCTTAAGGTAAACAAGGAGGAGACCTTTGCCATTGTTGGGATATT 180
DB 174 CACATACCGTAAAGCTTAAGGTAAACAAGGAGGAGACCTTTGCCATTGTTGGGATATT 233
QY 181 TTGTACCAACAATTTCAATAGGAAGCAAGGTATATGTCAAGACCTTGCCGACATACCA 240
DB 234 TTGTACCAACAATTTCAATAGGAAGCAAGGTATATGTCAAGACCTTGCCGACATACCA 293
QY 241 GACATATAAAGCGTCATTTCCGTAAGGATTTAAATGGGAAAGGCTATGAACCTTGAA 300
DB 294 GACATATAAAGCGTCATTTCCGTAAGGATTTAAATGGGAAAGGCTATGAACCTTGAA 353
QY 301 GACGCTGCGTCGTTACTGTAAACCGAGATTCAGATTGACAGATGCGTGTTCATCTAC 360
DB 354 GACGCTGCGTCGTTACTGTAAACCGAGATTCAGATTGACAGATGCGTGTTCATCTAC 413

QY 361 AAGTCAGTTCAATTGGCGTGAACCTTTCCTCCGATGAGACCTGTATGCAAAAGAGACA 420
DB 414 AAGTCAGTTCAATTGGCGTGAACCTTTCCTCCGATGAGACCTGTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAGACGACGACTGAGCGCTTGTATCTCGTATGAGCGCGTGTGAAGAGAG 480
DB 474 ATGGGCTGGGAGACGACGACTGAGCGCTTGTATCTCGTATGAGCGCGTGTGAAGAGAG 533
QY 481 ATTCAATAGGCTCTGAAGCTGAAGACCGTGTGTCATTACTTACCTAGTTGAATTCAAAGTATT 540
DB 534 ATTCAATAGGCTCTGAAGCTGAAGACCGTGTGTCATTACTTACCTAGTTGAATTCAAAGTATT 593
QY 541 TACATGGCAAAAGACCTGTGACGATACCGAGGATACCTAATGTTGATCTGCAACCTGAT 600
DB 594 TACATGGCAAAAGACCTGTGACGATACCGAGGATACCTAATGTTGATCTGCAACCTGAT 653
QY 601 ATACAGAGCCACAGACGAACTATACATGCTTGAGAGATGATAAGAACCGAGAGACGC 660
DB 654 ATACAGAGCCACAGACGAACTATACATGCTTGAGAGATGATAAGAACCGAGAGACGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731
RESULT 6
AX463698 859 bp DNA linear PAT 15-JUL-2002
LOCUS Sequence 12 from Patent WO0248338.
DEFINITION AX463698
ACCESSION AX463698.1 GI:21886457
VERSION
KEYWORDS
SOURCE
ORGANISM Discosoma sp.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia; Discosomatidae; Discosoma.
REFERENCE 1
Lichenberg-Frat, H.
TITLE Yeast strain for testing the geno- and cytotoxicity of complex environmental contamination
JOURNAL Patent: WO 0248338-A 12 20-JUN-2002;
Lichenberg-Frat, Hella (DE)
FEATURES
SOURCE Location/Qualifiers
1..859
/organism="Discosoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"
54..731
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD42147.1"
/db_xref="GI:21886458"
/db_xref="REWIREMBL:CAD42147"
/translation="MRSKNVLEKEMRPFVMEGTVNGHEFEIEGEGRPYEGHNTV
KLKVTGGPILPFAWDILSPQYGSKYVYKHADIPDYKLSPEGFKEWVNFEDG
GVATVTDSSLDQGCFTYKVFIGNPDSQVPMQKTKGMEASTERYLPDQVLGE
IHKALKIKDGGHYLVEFKSIYMAKKPQVLPGYVYVDSKLDITSHNEDYTIIVEQYERIE
GRHHLFL"
ORIGIN
Query Match 100.0%; Score 678; DB 6; Length 859;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGATTGATGAGTTTAAAGTTGCGATGGAAGA 60
DB 54 ATGAGGCTTCCAGAAATGTTATCAAGAGATTGATGAGTTTAAAGTTGCGATGGAAGA 113
QY 61 ACGGTCATGGGCGACGATTTGAAATAGAAAGCCAGAGAGGAGGAGCCATAGGAAGC 120
DB 114 ACGGTCATGGGCGACGATTTGAAATAGAAAGCCAGAGAGGAGGAGCCATAGGAAGC 173
QY 121 CACATACCGTAAAGCTTAAGGTAAACAAGGAGGAGACCTTTGCCATTGTTGGGATATT 180

Db	174	CACAAATACCGTAAGCTTTAAAGGTAAACCAAGGGGGAGCCTTTGGCATTGGCTTGGGATATT	233
QY	181	TTGTACCAACAATTTCAAGTATGGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA	240
Db	234	TTGTACCAACAATTTCAAGTATGGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA	293
QY	241	GACTATATAAAGCTGTCAATTTCTCGAAGGATTTAAATGGAAAGGGTCATGAATCTTGA	300
Db	294	GACTATATAAAGCTGTCAATTTCTCGAAGGATTTAAATGGAAAGGGTCATGAATCTTGA	353
QY	301	GACGGTGGCGCTGTACTGTATACCAAGATTCAGTTTGACAGATGGCTGTTTCAATCTAC	360
Db	354	GACGGTGGCGCTGTACTGTATACCAAGATTCAGTTTGACAGATGGCTGTTTCAATCTAC	413
QY	361	AAGGTCAAGTTCATTGGCGGTGAACCTTCCCTCCGATGGACCGGTATGCCAAAGAAAGCA	420
Db	414	AAGGTCAAGTTCATTGGCGGTGAACCTTCCCTCCGATGGACCGGTATGCCAAAGAAAGCA	473
QY	421	ATGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTGAATGGCGTGTGGAAGAGAG	480
Db	474	ATGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTGAATGGCGTGTGGAAGAGAG	533
QY	481	ATTCTAAGGCTCTGAAGCTGAAGAACGGTGGTCAATTACCTAGTTGAATTCAAAAGTAT	540
Db	534	ATTCTAAGGCTCTGAAGCTGAAGAACGGTGGTCAATTACCTAGTTGAATTCAAAAGTAT	593
QY	541	TACATGGCAAGAAAGCTGTGACGTACCAAGGATCTACTATGTTGACTCCCAACTGAT	600
Db	594	TACATGGCAAGAAAGCTGTGACGTACCAAGGATCTACTATGTTGACTCCCAACTGAT	653
QY	601	ATAACAAAGCCCAACGAAGACTATATCATTCGTTGACAGTATGAAGAACCGAAGGAGCG	660
Db	654	ATAACAAAGCCCAACGAAGACTATATCATTCGTTGACAGTATGAAGAACCGAAGGAGCG	713
QY	661	CACCATCTGTTCTTTAA 678	
Db	714	CACCATCTGTTCTTTAA 731	

LOCUS	AX348043	666 bp	DNA	linear	PAT 06-FEB-2002
DEFINITION	Sequence 22 from Patent EP1172375.				
ACCESSION	AX348043				
VERSION	AX348043.1				
KEYWORDS	GI:18614153				
SOURCE	.				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Odenthal, M. and Jung, D.				
TITLE	Gene expression, genome alteration and reporter gene expression in myofibroblasts and myofibroblasts-like cells by using the regulatory regions within the alpha smooth muscle alpha-actin gene Patent: EP 1172375-A 22 16-JAN-2002;				
JOURNAL	Odenthal, Margarete (DE)				
FEATURES	Location/Qualifiers				
source	1..666				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Red Fluorescent Protein"				
ORIGIN					

Qy	13	AAGAAATGTTAACAAGAGATTCAATGAGGTTTAAAGTTCCGATCGAAGAAACGTCAATGGG	72
Db	1	AAGAAATGTTAACAAGAGATTCAATGAGGTTTAAAGTTCCGATCGAAGAAACGTCAATGGG	60
Matches	665	Conservative	0
Mismatches	0	Indels	0
Gaps	0		
Query Match	98.1%	Score 665	DB 6
Best Local Similarity	100.0%	Pred. No. 5e-186	Length 666

OY	73	CACAGATTGAAATPAGAAAGGAAAGAGAGGGGAGGCGCATTCGAAGCGCACAATACCGTA	132
Db	61	CACAGATTGAAATPAGAAAGCGGAGAGAGGGGAGCGCATTCGAAGCGCACAATACCGTA	120
OY	133	AAGCTTAAGTAAACCAAGGGGGGACCTTTGGCATTTGCTTGGATTAATTTGTCCACCAAA	192
Db	121	AAGCTTAAGTAAACCAAGGGGGGACCTTTGGCATTTGCTTGGATTAATTTGTCCACCAAA	180
OY	193	TTTCAGTATGGAGCAAGTATATGTACAGACCTTCGCCATATCCAGACTATATAAAG	252
Db	181	TTTCAGTATGGAGCAAGTATATGTACAGACCTTCGCCATATCCAGACTATATAAAG	240
OY	253	CTGTCAATTCCTCGAAGATTTAAATGGGAAAGGGTCATGAACTTTGAAAGCGGTGGCGTC	312
Db	241	CTGTCAATTCCTCGAAGATTTAAATGGGAAAGGGTCATGAACTTTGAAAGCGGTGGCGTC	300
OY	313	GTTACTGTAAACCCAGATTCCTCGATTTGCAGATGGCTGTTTCATCTACAGSTCAAGTTC	372
Db	301	GTTACTGTAAACCCAGATTCCTCGATTTGCAGATGGCTGTTTCATCTACAGSTCAAGTTC	360
OY	373	ATTGGCGTGAACTTTCTCTCCGATGAACTGTATTCGAAAAGAAACATGGGCTGGGAA	432
Db	361	ATTGGCGTGAACTTTCTCTCCGATGAACTGTATTCGAAAAGAAACATGGGCTGGGAA	420
OY	433	GCCAGCACTGAGCGTTTGTATCCTCGATGAGCGGTGTTGAAAAGAGATTCATPAAGCT	492
Db	421	GCCAGCACTGAGCGTTTGTATCCTCGATGAGCGGTGTTGAAAAGAGATTCATPAAGCT	480
OY	493	CTGAAAGCTGAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAGTATTTACATGGCAAG	552
Db	481	CTGAAAGCTGAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAGTATTTACATGGCAAG	540
OY	553	AAGCCTGTGACCTACCAAGGTACTATATGTTGACTCCAACTGGATATTAACAAGCCAC	612
Db	541	AAGCCTGTGACCTACCAAGGTACTATATGTTGACTCCAACTGGATATTAACAAGCCAC	600
OY	613	AACGAAGACTATACATCTGTTGACACTATGAAAGAACCAAGGGAGCCCAACCATCTGTC	672
Db	601	AACGAAGACTATACATCTGTTGACACTATGAAAGAACCAAGGGAGCCCAACCATCTGTC	660

RESULT 8			
LOCUS	AX353910	666 bp	DNA
DEFINITION	Sequence 22 from Patent WO0204509.		linear
ACCESSION	AX353910		
VERSION	AX353910.1		
KEYWORDS	GI:1861888		
SOURCE			
ORGANISM	synthetic construct		
	artificial sequences.		
REFERENCE	1		
AUTHORS	Odenthal, M. and Jung, D.		
TITLE	Gene expression, genome alteration and reporter expression in myofibroblasts and mycibibroblast-like cells		
JOURNAL	Patent: WO 0204509-A 22 17-JAN-2002;		
	Odenthal, Margarette (DE)		
FEATURES	Location/Qualifiers		
Source	1..666		
	/organism="synthetic construct"		

ORIGIN	/note="Red Fluorescent Protein"
Query Match	98.1%; Score 665; DB 6; Length 666;
Best Local Similarity	100.0%; Pred. No. 5e-186;
Matches 665; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY	13	AAAGATGTTATCAACAGACTTCATGAGGTTTAAAGTTGCGATGGAAGGAACGGTCAATGGG	72
Db	1	AAGATGTTATCAACAGAGTTCAAGGGTTTAAAGTTGCGATGGAAGGAACGGTCAATGGG	60
QY	73	CACGAGTTTGAATATGAAGGCGCAAGAGAGGGGAGGCCATACGAAGCCACATATCCGTA	132
Db	61	CACGAGTTTGAATATGAAGGCGCAAGAGAGGGGAGGCCATACGAAGCCACATATCCGTA	120
QY	133	AAAGCTTAAGGTAAACCAAGGGGGGAGCCTTTGGCATTTGCTTGGGATATTTTGTCAACACAA	192
Db	121	AAAGCTTAAGGTAAACCAAGGGGGGAGCCTTTGGCATTTGCTTGGGATATTTTGTCAACACAA	180
QY	193	TTTCAGTATGGAAGCAAGGTATATGTCAAGCAACCCCTGCGACATATCCAGACTATAAAAAG	252
Db	181	TTTCAGTATGGAAGCAAGGTATATGTCAAGCAACCCCTGCGACATATCCAGACTATAAAAAG	240
QY	253	CTGTCAATTTCTCGAAGGATTTTAAATGGGAAAAGGTCATGAACCTTTGAAGACGGTGGCGTC	312
Db	241	CTGTCAATTTCTCGAAGGATTTTAAATGGGAAAAGGTCATGAACCTTTGAAGACGGTGGCGTC	300
QY	313	GTTACTGTAAACCCAGAGATTTCCAGTTTGCAGGATGGCTGTTTCATCTAACAAAGTCAAGTTC	372
Db	301	GTTACTGTAAACCCAGAGATTTCCAGTTTGCAGGATGGCTGTTTCATCTAACAAAGTCAAGTTC	360
QY	373	ATTGSCGTGAACCTTTCTTCGATGGAACCTGTTATGCAAAAAGAAAGACATGGGCTGGGAA	432
Db	361	ATTGSCGTGAACCTTTCTTCGATGGAACCTGTTATGCAAAAAGAAAGACATGGGCTGGGAA	420
QY	433	GCCAGCACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAGATTCATTAAGGCT	492
Db	421	GCCAGCACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAGATTCATTAAGGCT	480
QY	493	CTGAAGCTGAAAAGAGGGTGTCAATTAAGTAAATTCAAAAGATTTAATATGAGCAAG	552
Db	481	CTGAAGCTGAAAAGAGGGTGTCAATTAAGTAAATTCAAAAGATTTAATATGAGCAAG	540
QY	553	AAGCTGTGACAGCTACCAAGGGTACTATGTGTGAATCTCAAACTGGATATTAACAAGCCAC	612
Db	541	AAGCTGTGACAGCTACCAAGGGTACTATGTGTGAATCTCAAACTGGATATTAACAAGCCAC	600
QY	613	AACGAAGCTATACATGCTGTTGAGCAGTATGAAAGAACCGAGGGAGCGCACCATCTGTTTC	672
Db	601	AACGAAGCTATACATGCTGTTGAGCAGTATGAAAGAACCGAGGGAGCGCACCATCTGTTTC	660
QY	673	CTTTA 677	
Db	661	CTTTA 665	
RESULT 9			
LOCUS	AX686888	898 bp	DNA
DEFINITION	Sequence 11 from Patent WO0127150.		linear
ACCESSION	AX686888		
VERSION	AX686888.1		GI:29409468
KEYWORDS			
SOURCE			
ORGANISM			
			Discosoma sp.
			Discosoma sp.
			Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
			Coralimorpharia; Discosomellidae; Discosoma.
REFERENCE			
AUTHORS	1		
TITLE			lukyanov,S.A., Fradkov,A.F., Labas,Y.A., Matz,M.V. and Teriskikh,A.
			Anthozoa derived chromo/fluoroproteins and methods for using the
JOURNAL			same
FEATURES			Patent: WO 0127150-A 11 19-APR-2001;
source			Clontech Laboratories Inc. (US)
			location/Qualifiers
			1..898
			/organism="Discosoma sp."
			/mol_type="unassigned DNA"
			/db_xref="taxon:86600"
ORIGIN			

Query Match	97.2%;	Score 658.8;	DB 6;	Length 898;
Best Local Similarity	-98.2%;	Pred. No. 3.5e-184;		
Matches 666;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

OY	1	ATGAGGTCTTCCAAAGAATGGTTATACAGAGTTCATGAGTTTAAGGTTTAGGTTTCGATCGAAGA	60
Db	93	ATGAGGTCTTCCAAAGAATGGTTATCAAGAGTTTCATGAGTTTAAGGTTTCGATCGAAGA	152
OY	61	ACGGTCATGEGGCACGATTGGAAATGAAGCGAACAGAGGGGAGGCCATACGAAGGC	120
Db	153	ACGGTCATGEGGCACGATTGGAAATGAAAGCACAAGAGAGGGAGGCCCATACGAAGGC	212
OY	121	CACATAACCGTAAGACTTAAGTAAACAGAGGGGGACCCTTGCCATTTGCTTGGGATAAT	180
Db	213	CACATAACCGTAAGCTTAAGGTAAACCAAGGGGGACCCTTGCCATTTGCTTGGGATAAT	272
OY	181	TTGTACACCAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTTGCCGCAATACCA	240
Db	273	TTGTACACCAATTTCAGTATGGAAGCAGGTAATATGTCAAGCACCTTGCCGCAATACCA	332
OY	241	GACTATAAAAAGCTGTCAATTCCTGAAGAGATTTAAATGGGAAAAGGTCATGACTTTGA	300
Db	333	GACTATAAAAAGCTGTCAATTCCTGAAGAGATTTAAATGGGAAAAGGTCATGACTTTGA	392
OY	301	GACGGTGGCGTCTTACTGAACCCAGAGATTCAGTTTGACAGATGGCTGTTTCATCTAC	360
Db	393	GACGGTGGCGTCTTACTGAACCCAGAGATTCAGTTTGACAGAGTGGCTGTTTCATCTAC	452
OY	361	AAGGTCAAGTTCATTTGGCGTGAACCTTTCCTCCGATGGACCTGATTAAGCAAAGAAGCA	420
Db	453	AAGTCAAGTTATTTGGCGTTGAACCTTTCCTCCGATGGACCTGATTAAGCAAAGAAGCA	512
OY	421	ATGGGCTGGGAAGCAGACACTGAGCGTTTGTATCCTCGTGAATGGCGTTTGAAGAAGAG	480
Db	513	ATGGGCTGGGAAGCAGACACTGAGCGTTTGTATCCTCGTGAATGGCGTTTGAAGAAGAG	572
OY	481	ATTCTAATAGGCTCTGAAGCTGAAGAACGATGGTCTATTAACCTAAGTTGAATTAAGAATTT	540
Db	573	ATTCTAATAGGCTCTGAAGCTGAAGAACGATGGTCTATTAACCTAAGTTGAATTAAGAATTT	632
OY	541	TACATGGCAAGAAGCTGTGCAGCTACACAGGTACTACTATGTTGATCCCAACTGGAT	600
Db	633	TACATGGCAAGAAGCTGTGCAGCTACACAGGTACTACTATGTTGATCCCAACTGGAT	692
OY	601	ATTAACAGCCCAACGAAGACTATACATGCTTTGACAGTATGAAGAACCAGAGGAGCG	660
Db	693	ATTAACAGCCCAACGAAGACTATACATGCTTTGACAGTATGAAGAACCAGAGGAGCG	752
OY	661	CACCATCTGTTCCCTTTAA	678
Db	753	CACCATCTGTTCCCTTTAA	770

RESULT 10				
AF272711				
LOCUS	AF272711	876 bp	mRNA	linear
DEFINITION	Discosoma sp. SSAL-2000 red fluorescent protein (FP953) complete cds.			INV 26-SEP-2000
ACCESSION	AF272711			
VERSION	AF272711.1	GI:10304306		
KEYWORDS				
SOURCE				
ORGANISM	Discosoma sp. SSAL-2000			
	Discosoma sp. SSAL-2000			
	Eukaryota; Metazoa; Cnidaria; Anthozoa; Scleractinia; Corallimorpharia; Discosomatidae; Discosoma.			
REFERENCE	1 (bases 1 to 876)			
AUTHORS	Bradkov,A.F., Chen,Y., Ding,L., Barrova,E.V., Matz,M.V. and Lukyanov,S.A.			
TITLE	Novel fluorescent protein from Discosoma coral and its mutants possesses a unique far-red fluorescence			
JOURNAL	FEBS Lett. 479 (3), 127-130 (2000)			
MEDLINE	20434599			
PubMed	10981720			

REFERENCE 2 (bases 1 to 876)
AUTHORS Fradkov,A.F., Chen,Y., Ding,L., Barsova,E.V., Matz,M.V. and Lukyanov,S.A.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-2000) Institute of Bioorganic Chemistry RAS, Mklukho-Maklaya 16/10, Moscow 117811, Russia
FEATURES
source
1..876
/organism="Discozoma sp. SSAL-2000"
/mol_type="mRNA"
/db_xref="taxon:137428"
1..876
/gene="FP593"
45..737
/gene="FP593"
/note="defp593"
/codon_start=1
/product="red fluorescent protein"
/protein_id="PAG16224.1"
/db_xref="GI:10304307"
/translation="MCSRNVVKEFMRFKYRMETGVNGHFEIKGEGRPYRHCSEV KLMVTKGPIPAFDILSPQYSGKYVHPADIPIYKLSPEEGKMRVNMLEDG GVTVSODSLKDGSCFIVEKFIGVNPSPDQVORRTGMEASSEELYPDDTKGD IHMAIRREGSHIVFERKSIYMKKPSVQLPGITYDSKIDMTSHNEDYIVVEQYEXT QGRHPIKPLQ"

ORIGIN
Query Match 83.5%; Score 566.4; DB 3; Length 876;
Best Local Similarity 90.6%; Pred. No. 9.5e-157;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGAGGCTCTCCAGAAATGTTATCAGAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 60
DB 45 ATGAGTGTTCAGAAATGATGATCAAGAGTTTCATGAGTTTCGATGAAAGA 104
QY 61 ACGGTCAATGGGCGAGTTTGAATGAAAGGCAAGAGAGGAGGAGCCATACGAAGC 120
DB 105 ACGGTCAATGGGCGAGTTTGAATGAAAGGCAAGAGAGGAGGAGCCTTACGAAGT 164
QY 121 CACAATACCGTAAAGCTTAAAGGTAAACAAAGGAGGAGCCTTGCATTTGGGATATT 180
DB 165 CAGCTTCCTGTAAGCTTAAGTAAAGGTAACAAAGGAGGAGCCTTGCATTTGGATATT 224
QY 181 TTGTACACCAATTTCAATGTAAGAGCAAGGTATATGTCAAGCAGCTGCGACATACCA 240
DB 225 TTGTACACCAATTTCAATGTAAGAGCAAGGTATATGTCAAGCAGCTGCGACATACCA 284
QY 241 GACTATATAAAGCTGTATTTCTGAAAGATTAAATGGGAAAGGTCATGAATTGGAA 300
DB 285 GACTATATAAAGCTGTATTTCTGAAAGATTAAATGGGAAAGGTCATGAATTGGAA 344
QY 301 GACGATGAGGCTGTTACTGTAAACCAAGATTCAGATTGCGAGATGCTGTTTCATCTAC 360
DB 345 GACGATGAGGCTGTTACTGTAAACCAAGATTCAGATTGCGAGATGCTGTTTCATCTAC 404
QY 361 AAGGTCAAGTTCAATGAGCTGTAACCTTCCGATGAGAGCCTGTTATGCAAAAGACACA 420
DB 405 GAGGTCAAGTTCAATGAGCTGTAACCTTCCGATGAGAGCCTGTTATGCAAGAGACACA 464
QY 421 ATGGGGCTGGGAAGCCAGACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAG 480
DB 465 CGGGGCTGGGAAGCCAGACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAG 524
QY 481 ATTCAATAGGCTGGAAGCTGAAAGAGCGTGTGATTAACCTAGTTGAATCAAAAGATT 540
DB 525 ATCCATATGGCTCTGAGGCTGGAGAGAGCGGCCATTAACCTGTTGAATTCAAAAGATT 584
QY 541 TACATGCAAAAGAGCCT--GTGACGCTACCAAGGTAATACTATGTTGACTCCAAATG 597
DB 585 TACATGTAAGAGAGCCTTCAAGTGCAGGTGCAGGTATATATGTTGACTCCAAATG 644
QY 598 GATTATCAAGCCCAAGAGAGCTATATACATGTTGAGCATGTGAAAGAGCCGAGGGA 657

DB 645 GATTATCAAGCCCAAGAGAGTTACACAGTGTGAGCATGTATGAAAAACCCAGGGA 704
QY 658 CGCCACCATCTGTTCTTTA 677
DB 705 CGCCACCATCTGTTCAATTA 724
RESULT 11
AX686894 876 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 17 from patent WO0127150.
DEFINITION AX686894
ACCESSION AX686894
VERSION AX686894.1 GI:29409472
KEYWORDS
SOURCE
ORGANISM
Discozoma sp.
Discozoma sp.
Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia;
Corallimorpharia; Discosomatidae; Discozoma.
REFERENCE
AUTHORS Lukyanov,S.A., Fradkov,A.F., Labas,Y.A., Matz,M.V. and Teresikh,A.
TITLE Anthozoa derived chromo/fluoroproteins and methods for using the same
JOURNAL Patent: WO 0127150-A 17 19-APR-2001;
Clontech Laboratories Inc. (US)
FEATURES
source
1..876
/organism="Discozoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"

ORIGIN
Query Match 83.5%; Score 566.4; DB 6; Length 876;
Best Local Similarity 90.6%; Pred. No. 9.5e-157;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGAGGCTCTCCAGAAATGTTATCAGAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 60
DB 45 ATGAGTGTTCAGAAATGATGATCAAGAGTTTCATGAGTTTCGATGAAAGA 104
QY 61 ACGGTCAATGGGCGAGTTTGAATGAAAGGCAAGAGGAGGAGCCATACGAAGC 120
DB 105 ACGGTCAATGGGCGAGTTTGAATGAAAGGCAAGAGGAGGAGCCTTACGAAGT 164
QY 121 CACAATACCGTAAAGCTTAAAGGTAAACAAAGGAGGAGCCTTGCATTTGGGATATT 180
DB 165 CAGCTTCCTGTAAGCTTAAGTAAAGGTAACAAAGGAGGAGCCTTGCATTTGGATATT 224
QY 181 TTGTACACCAATTTCAATGTAAGAGCAAGGTATATGTCAAGCAGCTGCGACATACCA 240
DB 225 TTGTACACCAATTTCAATGTAAGAGCAAGGTATATGTCAAGCAGCTGCGACATACCA 284
QY 241 GACTATATAAAGCTGTATTTCTGAAAGATTAAATGGGAAAGGTCATGAATTGGAA 300
DB 285 GACTATATAAAGCTGTATTTCTGAAAGATTAAATGGGAAAGGTCATGAATTGGAA 344
QY 301 GACGATGAGGCTGTTACTGTAAACCAAGATTCAGATTGCGAGATGCTGTTTCATCTAC 360
DB 345 GACGATGAGGCTGTTACTGTAAACCAAGATTCAGATTGCGAGATGCTGTTTCATCTAC 404
QY 361 AAGGTCAAGTTCAATGAGCTGTAACCTTCCGATGAGAGCCTGTTATGCAAAAGACACA 420
DB 405 GAGGTCAAGTTCAATGAGCTGTAACCTTCCGATGAGAGCCTGTTATGCAAGAGACACA 464
QY 421 ATGGGGCTGGGAAGCCAGACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAG 480
DB 465 CGGGGCTGGGAAGCCAGACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAG 524
QY 481 ATTCAATAGGCTGGAAGCTGAAAGAGCGTGTGATTAACCTAGTTGAATCAAAAGATT 540
DB 525 ATCCATATGGCTCTGAGGCTGGAGAGAGCGGCCATTAACCTGTTGAATTCAAAAGATT 584
QY 541 TACATGCAAAAGAGCCT--GTGACGCTACCAAGGTAATACTATGTTGACTCCAAATG 597

Db 585 TACATGTAAAGAAAGCTTCAGTCAGTGTCCAGGCTACATATATGTTGACTCCAAACTG 644

Qy 598 GATATTAACAAGCCCAACGAAGACTATACATTCGTTAGAGCATGAAAGAACGAGGGA 657

Db 645 GATATGAGAGCCCAACGAAGATTACAGTCTGTAGCATATGAAAAAACCAAGGGA 704

Qy 658 CGCCACCATCTGTTCTTTA 677

Db 705 CGCCACCATCTGTTCTTTA 724

RESULT 12

AX233584 681 bp DNA linear PAT 11-SEP-2001

LOCUS AX233584

DEFINITION Sequence 8 from Patent WO0162919.

AX233584

AX233584.1 GI:15593307

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

artificial sequences.

REFERENCE

1 Nelson, D., Zamaira, E. and Tsien, R.

AUTHORS Modified fluorescent proteins

TITLE Patent: WO 0162919-A 8 30-AUG-2001;

JOURNAL Aurora Biosciences Corporation (US)

FEATURES

source

1. .681

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Mutant Anthozoan red fluorescent protein"

1. .681

/note="unnamed protein product"

/codon_start=1

/transl_table=11

/protein_id="CAC69734.1"

/db_xref="GI:15593308"

/db_xref="REMBL:CAC69734"

/translation="MVRSSKNVKEFMRFKRMGTVNGHEFEIEGEGRHYEHNHT

VKLRVTKGSLPAMVDILSPQFGSKVYVGPADIPYKLSPEPGKRMVNFED

GVVTVNDSSIQGCFYKYKFTGVNPSGPMOKMTWEMASTRLYVRDVLG

EIHAKLKDGDGHVLEFKSIYMAKVPQLFGYIVDSKLDITSHNEDYITVEQYERT

EGRHHLFL"

ORIGIN

Query Match 66.3%; Score 449.8; DB 6; Length 681;

Best Local Similarity 79.0%; Pred. No. 3.9e-122;

Matches 535; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 2 TGAAGCTCTCCAGAATGTTATCAAGAGTTTCATGAGGTTTAAAGTTTCGATGGAAGAA 61

Db 5 TGAAGAGCAGCAAGACGTATCAAGAGTTTCATGAGGTTTCAAGGTGCGCATGAGAGGCA 64

Qy 62 CGGTCAATGGGCAAGAGTTTAAATGAAAGGGAAGAGAGGAGGCGCATACGAAGGCC 121

Db 65 CGGTGAAGGGCCACAGTTTCAGATCGAGGGGAGAGGGGCGAGGCGCTTACGAGGCC 124

Qy 122 ACAATACCGTAAAGCTTAAAGTTAACCAAGGGGGAGACTTTGGCATTTCTTGGGATATTT 181

Db 125 ACAACACCGTGAAGCTTAAAGTTAGACCAAGGGGGGCGCCCTGCTTCCGCTGGGACATCC 184

Qy 182 TGTCAACAATTTTCAGTATGGAAGCAAGTATATGTCAAGACCCCTGCGCATATACAG 241

Db 185 TGAGCCCCAGTTTCAGTACGCGCAAGAGTGTATGTAAGCAACCCGCGCATATCCCG 244

Qy 242 ACTATAAAAAGCTGATTTCTGAAAGATTTAAATGGGAAAGGTCATGAATCTTGAAG 301

Db 245 ACTACAAAGAGCTGAGCTTCCCGAGGGCTTCAATGGGAGAGGTTGATGAATTCGAGG 304

Qy 302 ACGGTGGGCTGTTCTGTAAACCAAGATTTCAGATTTGAGAGATGGCTGTTTCATCTCA 361

Db 305 ACGGCGGGCTGTGACCTGACCCAGACAGACGCTGTGAGGACGGCTGCTTCACTTACA 364

Qy 362 AGCTCAAGTTCAATTGGCTGAACCTTTCCTTCGATGAGACTGTATTCCAAAGAACCA 421

Db 365 AGGTGAAGTTCAATCGGGTGAACCTTCCCGACAGCGCCCCGATGACAAAGAACCA 424

Qy 422 TGGGCTGGGAAGCAGCAGTGAAGGTTTGTATCTGCTGATGGCGTTGAAAGAGAGA 481

Db 425 TGGGCTGGAGGCTTCCACGAGGCTGTATCCCGCAGCGGCTGCTAAGAGGCGAGA 484

Qy 482 TTCAATAGGCTCTGAAGCTGAAGAACGAGTGTATTAAGTTGAATTCAAAGATTTT 541

Db 485 TCACAAAGGCTCTGAAGCTGAAGAACGAGTGTATTAAGTTGAATTCAAAGATTTT 544

Qy 542 ACATGGCAAGAACCTGTGACGATACAGAGGTAATCTATGTTGACTCCAACTGGATA 601

Db 545 ACATGGCAAGAACCTGTGACGATACAGAGGTAATCTATGTTGACTCCAACTGGATA 604

Qy 602 TTAACAGCACAACGAAGACTATATCAATGTTAGAGTATGAAAGAACGAGGAGGCC 661

Db 605 TCACAGCACAACGAAGACTATATCAATGTTAGAGTATGAAAGAACGAGGAGGCC 664

Qy 662 ACCATCTGTTCTTTAA 678

Db 665 ACCATCTGTTCTTTAA 681

RESULT 13

AX233627 713 bp DNA linear PAT 11-SEP-2001

LOCUS AX233627

DEFINITION Sequence 51 from Patent WO0162919.

AX233627

AX233627.1 GI:15593330

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

synthetic construct

synthetic construct

artificial sequences.

REFERENCE

1 Nelson, D., Zamaira, E. and Tsien, R.

AUTHORS Modified fluorescent proteins

TITLE Patent: WO 0162919-A 51 30-AUG-2001;

JOURNAL Aurora Biosciences Corporation (US)

FEATURES

source

1. .713

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Mutant Anthozoan red fluorescent protein"

ORIGIN

Query Match 66.3%; Score 449.8; DB 6; Length 713;

Best Local Similarity 79.0%; Pred. No. 3.9e-122;

Matches 535; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 2 TGAAGCTCTCCAGAATGTTATCAAGAGTTTCATGAGGTTTAAAGTTTCGATGGAAGAA 61

Db 23 TGAAGAGCAGCAAGACGTATCAAGAGTTTCATGAGGTTTCAAGGTGCGCATGAGAGGCA 82

Qy 62 CGGTCAATGGGCAAGAGTTTGAATGAAAGGCGAAGAGAGGAGGCCATACGAAGGCC 121

Db 83 CGGTGAAGGGCCACAGTTTCAGATCGAGGGGCGAGAGGCGAGGCGCTTACGAAGGCC 142

Qy 122 ACAATACCGTAAAGCTTAAAGTTAACCAAGGGGGAGACTTTGGCATTTGCTTGGGATATTT 181

Db 143 ACAACACCGTGAAGCTTAAAGTTAGACCAAGGGGGGCGCCCTGCTTCCGCTGGGACATCC 202

Qy 182 TGTCAACAATTTTCAGTATGGAAGCAAGTATATGTCAAGACCCCTGCGCATATACAG 241

Db 203 TGAGCCCCAGTTTCAGTACGCGCAAGAGTGTATGTAAGCAACCCGCGCATATCCCG 262

Qy 242 ACTATAAAAAGCTGATTTCTGAAAGATTTAAATGGGAAAGGTCATGAATCTTGAAG 301

Db 263 ACTACAAAGAGCTGAGCTTCCCGAGGGCTTCAAGTGGGAGAGGTTGATGAATTCGAGG 322

QY 302 ACCGTGGCGTCTGTAAGTACCAAGATTCAGATTGCGAGATGGCTTTTCATCTTACA 361
DB 323 ACCGCGCGCTGTGTACCGGTGACCCAGACAGACCGCTGCGAGAGCGGCTGCTTCACTTACA 382
QY 362 AGGTCAAGTTCATTTGGCGTGAATCTTTCCGATGAGACCTGTATGCAAAAGAGACAA 421
DB 383 AGGTGAAGTTCATTTGGCGTGAATCTTTCCGATGAGACCTGTATGCAAAAGAGACCA 442
QY 422 TGGGCTGGGAGAGCCAGCACTGAGCGTTTGTATCTCTGTGATGGCGTTTGAAGAGAGA 481
DB 443 TGGGCTGGGAGAGCCAGCACTGAGCGCTGTATCTCTGTGATGGCGTTTGAAGAGAGA 502
QY 482 TTCTAAGGCTCTGTAAGTGAAGACCGGTGTCTTACTTACTTGAATTCAGAAATTTT 541
DB 503 TCCACAAAGGCGCTGTGAAGTGAAGACCGCGCCACTCTGTGTGAGTTCAAGTCCACTCT 562
QY 542 ACATGGCAAGAGAGCTGTGAGTACACAGGCTACTACTATGTTGATCTCCAAATGAGATA 601
DB 563 ACATGGCAAGAGAGCGGTGTGAGTCTGCGCGCTACTACTTACGTGACTCCAAAGTGAACA 622
QY 602 TAAACACCAACAAAGAGACTATACAACTGTTGAGCATATGAAAGAACCGAGGAGCGCC 661
DB 623 TCAACCAACCAACAAAGAGACTATACCACTGTTGAGCATATGAAAGAACCGAGGAGCGC 682
QY 662 ACCATCTGTTCTTTAA 678
DB 683 ACCACCTGTTCTGTGA 699

RESULT 14
AX370404 678 bp DNA linear PAT 16-FEB-2002

LOCUS AX370404
DEFINITION Sequence 1 from Patent WO0196373.
ACCESSION AX370404
VERSION AX370404.1 GI:18857490
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pradkov A.P. and Terzikikh A.
TITLE Fluorescent timer proteins and methods for their use
JOURNAL Patent: WO 0196373-A 1 20-DEC-2001;
Clontech Laboratories Inc. (US)
FEATURES
source location/Qualifiers
1..678
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="variant of sequence from *Discozoma* sp."

ORIGIN

Query Match 66.3%; Score 449.2; DB 6; Length 678;
Best Local Similarity 78.9%; Pred. No. 5.9e-122;
Matches 535; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
DB 1 ATGAGGCTTCCCAAGAACGTCATCAAGAGTTCATGAGTTTCGATGGAAGAGGC 60
QY 61 ACCGTCAATGGGCAAGATTGAATGAAGGCGAAGAGAGAGGAGGCGCATACGAAGGC 120
DB 61 ACCGTCAATGGGCAAGATTGAATGAAGGCGAAGAGAGAGGAGGCGCGCTACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CACAACACCGTGAAGCTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 TTGTCAACCAATTTAGTATGGAAGCAAGTATATGTCAGACACCTGCGCATACCA 240
DB 181 CTGTCCCCCGAGTTCCAGTACGAGTCCAGAGGTGACGTGAAGACACCCGCGCATATCCC 240
QY 241 GACTATATAAAGCTGCTATTTCTGGAAGATTAAATGGGAAGGAGTCAATGAACTTTGAA 300

DB 241 GACTATATAAAGCTGCTATTTCTGGAAGATTAAATGGGAAGGAGTCAATGAACTTTGAG 300
QY 301 GACGCGCGCTGCTTCTGTATACCAAGATTCAGATTGCGAGATGGCTTTTCATCTTAC 360
DB 301 GACGCGCGCTGCTTCTGTATACCAAGATTCCTTCTGTGAGAGACGCTTCTTATCTAC 360
QY 361 AAGTCAAGTTCATTTGGCGTGAATCTTTCCGATGAGACCTGTATGCAAAAGAGACA 420
DB 361 AAGTCAAGTTCATTTGGCGTGAATCTTTCCGATGAGACGCTTCTTATGCAAAAGAGACC 420
QY 421 AAGGCTGGGAGAGCCAGCACTGAGCGTTTGTATCTCTGTGATGGCGTTTGAAGAGAG 480
DB 421 AAGGCTGGGAGAGCCAGCACTGAGCGCTGTATCTCTGTGATGGCGTTTGAAGAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAAGTGAAGACCGGTGTCTATTAATCTTAATTAATTAATTT 540
DB 481 ATCCACAGGCGCTGAAAGTGAAGAGACCGGCGCACTACTGTGTGAAGTTCAAGTGCATC 540
QY 541 TACATGGCAAGAGAGCTGTGAGTACACAGGCTACTACTATGTTGAATCCAAATGAGAT 600
DB 541 TACATGGCAAGAGAGCGGTGTGAGTCTGCGCGCTACTACTTACGTGAGATCCAAAGTGAAC 600
QY 601 ATTAACAGCCACAAAGAGACTATACAACTGTTGAGCATATGAAAGAACCGAGGAGCGC 660
DB 601 ATCACTCCCAACAAAGAGACTATACCACTGTGAGCATATGAAAGAACCGAGGAGCGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCACCTGTTCTGTGA 678

RESULT 15
AX824725 678 bp DNA linear PAT 11-DEC-2003
LOCUS AX824725
DEFINITION Sequence 7 from Patent WO02068459.
ACCESSION AX824725
VERSION AX824725.1 GI:39750591
KEYWORDS
SOURCE *Discozoma* sp.
ORGANISM *Discozoma* sp.
REFERENCE 1
AUTHORS Bukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia;
TITLE Corallimorpharia; *Discozomidae*; *Discozoma*.
JOURNAL
FEATURES
source location/Qualifiers
1..678
/organism="Discozoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"

ORIGIN
Query Match 66.3%; Score 449.2; DB 6; Length 678;
Best Local Similarity 78.9%; Pred. No. 5.9e-122;
Matches 535; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
DB 1 ATGAGGCTTCCCAAGAACGTCATCAAGAGTTCATGAGTTTCGATGGAAGAGGC 60
QY 61 ACCGTCAATGGGCAAGATTGAATGAAGGCGAAGAGAGAGGAGGAGGCGCATACGAAGGC 120
DB 61 ACCGTCAATGGGCAAGATTGAATGAAGGCGAAGAGAGAGGAGGAGGCGCGCTACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CACAACACCGTGAAGCTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 TTGTCAACCAATTTAGTATGGAAGCAAGTATATGTCAGACACCTGCGCATACCA 240
DB 181 CTGTCCCCCGAGTTCCAGTACGAGTCCAGAGGTGACGTGAAGACACCCGCGCATATCCC 240

```
QY 241 GACTATATAAAAGCTGTCATTTCTGTAAGATTTAAATGGAAAGGTCATGAACTTTGAA 300
    |||||
Db 241 GACTATACAAGAGCTGTCTTCCCCGAGGGCTTCAAGTGGAGCGCGTATGAACTTCGAG 300
QY 301 GACCGTGGCGTCTGTAACCTGTAACCCAGATTCAGATTGCAAGATGGCTTTTCACTTAC 360
    |||||
Db 301 GACCGCGGCGTGTGACCGTGAACCGATCTCTCCGAGAGCGGCTGCTCATTTAC 360
QY 361 AAGGTCAAGTTCATTGGCGTGAACCTTCTTCCGATGAGCTGTATGCAAAAGAGACA 420
    |||||
Db 361 AAGGTGAAGTTCATTGGCGGTGAACCTTCCCTCCGAGGCCCCGTGATGCAAGAGAGACC 420
QY 421 ATGGGCTGGGAAAGCCAGACTGAGCGTTTGTATCTCTGTGATGGCGTGTGAAAGAGAG 480
    |||||
Db 421 ATGGGCTGGGAGGCTTCACCGAGGCGCTGTACCCCGCAGACGGCGTGTGAAGGGCGAG 480
QY 481 ATTCTAAGGCTCTGTAAGCTGAAGAAGCGTGTGCTATTACTAGTTGAATTCAAAAGTATT 540
    |||||
Db 481 ATCCACAAGGCCCTGAAGCTGAAGGACGCGGCCACTACTGTGTGAGTTCAAGTCCATC 540
QY 541 TACATGGCAAGAAGCTGTGAGGCTACAGGGTACTACTATGTTGACTCCAAACTGGAT 600
    |||||
Db 541 TACATGGCCAAAGAGCCCGTGAAGCTGCGCGCTACTACTAGTGAAGTCCAAAGCTGAGC 600
QY 601 ATTAACAGCCACAACGAAAGACTATACAAATCGTTGAGAGTATGAAAAGAACGAGGAGCGC 660
    |||||
Db 601 ATCACTCTCCACAACGAGAGACTACACATCGTGAGAGTACGAGCGCACCGAGGGCGCGC 660
QY 661 CACCATCTGTCTCTTTAA 678
    |||||
Db 661 CACCACCTGTCTCTGTAA 678
```

Search completed: July 11, 2004, 10:35:31
Job time : 2085 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 09:50:20 ; Search time 66 Seconds
(without alignments)
5700.859 Million cell updates/sec

Title: US-10-006-922a-11

Perfect score: 678
Sequence: 1 atgaggcttcacaagaatg.....gccaccatcttctttaa 678

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1_0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptocdata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptocdata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptocdata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptocdata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptocdata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptocdata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	4	US-09-459-956-6
2	409.6	60.4	699	4	US-09-459-956-5
3	271	40.0	801	4	US-09-459-956-7
4	178.4	26.3	690	4	US-09-459-956-2
5	147.2	21.7	696	4	US-09-459-956-4
6	133.4	19.7	696	4	US-09-459-956-3
7	133.2	19.6	1079	4	US-09-609-1618-15
8	133.2	19.6	1079	4	US-09-626-581D-64
9	133.2	19.6	1079	4	US-09-415-765B-64
10	133.2	19.6	1079	4	US-09-626-580C-64
11	133.2	19.6	1085	3	US-09-277-716-15
12	132.4	19.5	1104	3	US-09-277-716-30
13	132.4	19.5	1104	4	US-09-609-1618-30
14	132.4	19.5	1279	3	US-09-277-716-31
15	132.4	19.5	1279	4	US-09-609-1618-31
16	130	19.2	1021	4	US-09-839-650-2
17	128.4	18.9	720	4	US-09-839-650-1
18	42	6.2	7218	4	US-08-232-463-14
19	34.4	5.1	2748	4	US-09-540-336-1106
20	34.4	5.1	19988	4	US-09-596-002-10
21	33.2	4.9	58073	4	US-08-545-528D-1
22	31.2	4.6	1098	4	US-09-716-793A-3
23	31.2	4.6	4100	4	US-09-620-312D-81
24	31	4.6	522	1	US-07-778-156-4
25	31	4.6	522	2	US-08-422-166-4
26	31	4.6	602	3	US-09-385-982-257
27	31	4.6	797	2	US-08-464-637-1

28	31	4.6	797	2	US-08-822-261-5	Sequence 5, Appl1
29	31	4.6	797	1	US-09-226-852-5	Sequence 5, Appl1
30	31	4.6	798	1	US-07-778-156-12	Sequence 12, Appl1
31	31	4.6	798	2	US-08-822-261-6	Sequence 6, Appl1
32	31	4.6	798	2	US-08-422-166-12	Sequence 12, Appl1
33	31	4.6	798	3	US-09-146-969-2	Sequence 2, Appl1
34	31	4.6	798	4	US-09-226-852-6	Sequence 6, Appl1
35	31	4.6	955	1	US-08-455-550-3	Sequence 3, Appl1
36	31	4.6	1002	4	US-08-271-948-1	Sequence 1, Appl1
37	31	4.6	1002	4	US-08-739-333-1	Sequence 1, Appl1
38	31	4.6	1002	4	US-09-754-105-1	Sequence 1, Appl1
39	31	4.6	1002	4	US-09-978-339-1	Sequence 1, Appl1
40	31	4.6	1002	5	PCT-US95-08534-1	Sequence 1, Appl1
41	31	4.6	1953	1	US-08-436-044-3	Sequence 3, Appl1
42	31	4.6	1953	2	US-08-436-054-3	Sequence 3, Appl1
43	31	4.6	1953	5	PCT-US95-08812-3	Sequence 3, Appl1
44	31	4.6	4342	1	US-08-436-044-1	Sequence 1, Appl1
45	31	4.6	4342	2	US-08-436-054-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-459-956-6
Sequence 6, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Taisen, Roger Y.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 678
TYPE: DNA
ORGANISM: Discosoma sp
US-09-459-956-6

Query Match 100.0%; Score 678; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGGCTTTCCCAAGAAATGTATCAAGAGCTTCATGAGTTTAAAGTTGGCATGGAAGA	60
DB	1	ATGAGGCTTTCCCAAGAAATGTATCAAGAGCTTCATGAGTTTAAAGTTGGCATGGAAGA	60
QY	61	ACGGTCAATGGGACGAGTTTGAATATGAAGGCAAGAGGAGGCGCATACGAAGGC	120
DB	61	ACGGTCAATGGGACGAGTTTGAATATGAAGGCAAGAGGAGGCGCATACGAAGGC	120
QY	121	CACATATCCGTAAGGTTTAAAGTTAACCAAGGGGAGCCTTTGCATTTCCTGGATATT	180
DB	121	CACATATCCGTAAGGTTTAAAGTTAACCAAGGGGAGCCTTTGCATTTCCTGGATATT	180
QY	181	TTGTCCCAATTTAGTATGGAAGCAAGATATGTAACGACCCCTCCGACATACCA	240
DB	181	TTGTCCCAATTTAGTATGGAAGCAAGATATGTAACGACCCCTCCGACATACCA	240
QY	241	GACTATTAAGAGTCTTCCTGAAGATTAAATGGAAGGTCATGAACCTTTGAA	300
DB	241	GACTATTAAGAGTCTTCCTGAAGATTAAATGGAAGGTCATGAACCTTTGAA	300

QY 301 GACGGTGGCTGTACTGTAAACCAAGATTCAGATTGCGAGATGCGTGTTCATCTAC 360
Db 301 GACGGTGGCTGTACTGTAAACCAAGATTCAGATTGCGAGATGCGTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCATGAGACCTGTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCATGAGACCTGTATGCAAAAGAGACA 420
QY 421 ATGGCTGGGAAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGGTGTGAAGAGAG 480
Db 421 ATGGCTGGGAAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGGTGTGAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAGCTGAAGAAGCGTGTCTATTCCTAGTGAATTCAGAAAGTAT 540
Db 481 ATTCAATAGGCTCTGAGCTGAAGAAGCGTGTCTATTCCTAGTGAATTCAGAAAGTAT 540
QY 541 TACATGGCAAGAACCTGTGCACTACCAAGGCTCTACTATGTGACTCCAACTGAT 600
Db 541 TACATGGCAAGAACCTGTGCACTACCAAGGCTCTACTATGTGACTCCAACTGAT 600
QY 601 ATACCAAGCCCAAGCAAGACTATACATCGTTGAGCATGAAAGAACCGAGGAGCG 660
Db 601 ATACCAAGCCCAAGCAAGACTATACATCGTTGAGCATGAAAGAACCGAGGAGCG 660
QY 661 CACCATCTGTCTCTTAA 678
Db 661 CACCATCTGTCTCTTAA 678

RESULT 2

US-09-459-956-5
Sequence 5, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Tsielen, Roger Y.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 699
TYPE: DNA
ORGANISM: *Dicosoma striata*
US-09-459-956-5

Query Match 60.4%; Score 409.6; DB 4; Length 699;
Best Local Similarity 76.2%; Pred. No. 1.4e-131;
Matches 518; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

QY 1 ATGAGTCTTCCAAAGATGTATCAAGAGTTCATGAGTTTAAAGTTGCGATGGAAGA 60
Db 1 ATGAGTCTTCCAAAGATGTATCAAGAGTTCATGAGTTTAAAGTTGCGATGGAAGA 60
QY 61 ACGGTCAATGGGCAAGAGTTGAATAGAGGCGAAGAGAGGAGGAGCCATACGAAGC 120
Db 61 ACGGTCAATGGGCAAGAGTTGAATAGAGGCGAAGAGAGGAGGAGCCATACGAAGC 120
QY 121 CACATATACCGTAAGCTTAAGTAAACAAAGGAGGAGCTTGTCCATTTGCTGGATAT 180
Db 121 CACATATACCGTAAGCTTAAGTAAACAAAGGAGGAGCTTGTCCATTTGCTGGATAT 180
QY 181 TTGTACCAACAATTTCAATATGGAAGCAAGGATATATGCAAGCAACCTGCGGACATACA 240
Db 181 TTGTACCAACAATTTCAATATGGAAGCAAGGATATATGCAAGCAACCTGCGGACATACA 240

Db 181 TTGTGCCCAAAATTTCAATATGGAAGCAAGGATTTGTCCACCACTGCAACATACAT 240
QY 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTTAAATGGAAAGGTCATGAACCTTTGAA 300
Db 241 GACTATATAAAGCTGTCAATTTCTGGAAGATTTAAATGGAAAGGTCATGAACCTTTGAA 300
QY 301 GACGCTGGCTGTACTGTAAACCAAGATTCAGATTGCGAGATGCGTGTTCATCTAC 360
Db 301 GACGCTGGCTGTACTGTAAACCAAGATTCAGATTGCGAGATGCGTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCATGAGACCTGTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCATGAGACCTGTATGCAAAAGAGACA 420
QY 421 ATGGCTGGGAAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGGTGTGAAGAGAG 480
Db 421 ATGGCTGGGAAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGGTGTGAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAGCTGAAGAAGCGTGTCTATTCCTAGTGAATTCAGAAAGTAT 540
Db 481 ATTCAATAGGCTCTGAGCTGAAGAAGCGTGTCTATTCCTAGTGAATTCAGAAAGTAT 540
QY 541 TACATGGCAAGAACCTGTGCACTACCAAGGCTCTACTATGTGACTCCAACTGAT 600
Db 541 TACATGGCAAGAACCTGTGCACTACCAAGGCTCTACTATGTGACTCCAACTGAT 600
QY 598 GATTAACAAGCCCAAGCAAGACTATACATCGTTGAGCATGAAAGAACCGAGGAG 657
Db 601 GTTATATGAACAACGCAAGAAATTCATGAAGATGAGAGCATGAATCGCGTTGCA 660
QY 658 CGCACCATCTGTCTCTTAA 677
Db 661 CGCACCATCTGTCTCTTAA 680

RESULT 3

US-09-459-956-7
Sequence 7, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Tsielen, Roger Y.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 801
TYPE: DNA
ORGANISM: *Clavularia sp*
US-09-459-956-7

Query Match 40.0%; Score 271; DB 4; Length 801;
Best Local Similarity 63.0%; Pred. No. 1.5e-83;
Matches 418; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 11 CCAAGATGTATCAAGAGTTCATGAGTTTAAAGTTGCGATGGAAGAGCGTCAATG 70
Db 125 CCAATGGTGTGATTAACCAAGCATGAAATTAAGCTGAAGATGAAAGAAATGTAAAG 184
QY 71 GGCACAGTTTGAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 130
Db 185 GGCATGTTTGTGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 244

OY	131	TTAAAGCTTAAGGTAACTAAAGGGGGGAACTTTGGCAATTTGCTTGGGATATTTTGTACACAC	190
Db	245	TAAACCTGAAAGTGAAGGAGGTGGCCCTCTGCTTTTCTTACGATCTTGTGAACG	304
OY	191	AATTTCACTATGGAAGCAAGGTATATGTTCAMGACCCCTGCGACATACCAACTATATAAA	250
Db	305	CGTTCACATGACGAAACAGAGCATTTGACAAATAATCCACAGACGATATAGCAGACTATTTCA	364
OY	251	AGCTGTCTTTTCTTGAAGATTTAATGGAAGAGGTGATGAACTTTGAAGACGGTGGG	310
Db	365	AGCACTCTTTTCCGAGGATATTTCTTGGGAAAGAACCTTGACTTTTGAAGCAAAAGCA	424
OY	311	TGCTTACTGTAAACCGAGATTCAGTTTGACAGATGCGCTGTTTCACTTCAAGTCAAGT	370
Db	425	TTGTCAAGTGAAGAAAGTACATTAACATGAGAGGAAGACCTCTTATCTATGAATTCGTT	484
OY	371	TCATTTGCGGTGAACTTTCTCTTCGATGACCTGTTATGCAAAAGAACATGCGCTGGG	430
Db	485	TTGATGGGATGAACCTTCTCTCCCAATGTCGCGGTATGACAGAAAAAACTTTGAAGTGGG	544
OY	431	AAGCAGACATGAGCGGTTTGTATCTCGATGAGGCGGTTTGAAGAGAGATTTCAATTAAG	490
Db	545	AACCATTCACATGAGATTTATGACGTGCGGTGATGAGATGCTGTCGAGATATTAAGCAAT	604
OY	491	CTCTGAACCTGAAGACGCGTGTCACTTACCTAGTTGAATTCAAAAGTATTTTACATGCA	550
Db	605	CTCTGTTCTGGAGGAGGTGGCCATTAACCGATGATCTTCAAAAGTATTTTCAAAAGCA	664
OY	551	AGAACCTGTGACGTACACAGGTACTACTATGTTGATCTCCAACTGATATTAACAAGC	610
Db	665	AAAAAGTTGTCAATTTGTCAGACTATCACTTTGTGACCATTCGATTCAGATCTTGAAAC	724
OY	611	ACAACGAAGACTATCAATTCGTTGACAGTATGAAGAAGACCGAGGAGCCGACCAATCTGT	670
Db	725	ATGACAAAGATTACAAACAAGTAAGCTGTATGAGATGCAATTTGCTGCTATTTCTTGC	784
OY	671	TCC 673	
Db	785	TGC 787	
RESULT 4			
US-09-459-956-2			
: Sequence 2, Application US/09459956			
: Patent No. 6342379			
: GENERAL INFORMATION:			
: APPLICANT: Tsien, Roger Y.			
: TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY			
: TITLE OF INVENTION: OPTICAL METHODS			
: FILE REFERENCE: REGEN1290-4			
: CURRENT APPLICATION NUMBER: US/09/459,956			
: CURRENT FILING DATE: 1999-12-13			
: PRIOR APPLICATION NUMBER: 08/765,860			
: PRIOR FILING DATE: 1999-05-08			
: PRIOR APPLICATION NUMBER: 08/481,977			
: PRIOR FILING DATE: 1995-06-07			
: PRIOR APPLICATION NUMBER: PCT/US96/09652			
: PRIOR FILING DATE: 1996-06-06			
: NUMBER OF SEQ ID NOS: 22			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 2			
: LENGTH: 690			
: TYPE: DNA			
: ORGANISM: Anemonia majano			
US-09-459-956-2			

	Query Match	26.3%	Score 178.4	DB 4	Length 690
	Best Local Similarity	56.1%	Pred. No. 1.6e-51		
	Matches 360	Conservative 0	Mismatches 276	Indels 6	Gaps 1
QY	9	TTCCAGAGTGTATTCACGAGCTTCATGAGCTTTAAGCTGCCATGAGAGAACGCTCA	68		

Db	9	TTCAAAACAGTTTATCGGAAGTGCATGAAAAATGACCTACCAATGATGATGGCTGTGTCAA	68
Oy	69	TGGGCGACGAGTTTGAATATGAAAGCCGAAGAGAGGGGACCATATCGAAGGCCACAAATAC	128
Db	69	TGGGCACTTATCTTATCCGTCAAAAGGTGAAGGCMAAGGGAAAGCCATACGAAGGGAACGCAAC	128
Oy	129	CGTAAAGCTTAAGGTA-----CCAAGGGGGAGACTTGTGCATTGTGGTATATTTT	182
Db	129	TTGCACCTTTAAATGCACATGGCCMAAGGTGGGCCCTTGCACTTCTCCTTTGACATACT	188
Oy	183	GTCACCACAATTTGATATGGAAGCAAGTATATGTCAAGACCCCTGCGCATACAGA	242
Db	189	ATCTACAGTGTCAAAATATGGAAATCGATGCTTACTGCGATCTCAAGATATGCCGA	248
Oy	243	CTATAAAAAGCTGCATTTCTCTGAAGATTTAAATGGGAAGGGTCATGAATTTGAAGA	302
Db	249	CTATTTCAACACAGCATTTTCTGTGAGGAATGTCAATGAAGAAGCATTTTACCTATGAAGA	308
Oy	303	CGGTGGCGTCGTATCTGTAAACCCAGAGATTCCAGTTTGCAGAGATGGCTGTTTCATCTACA	362
Db	309	TGAGAGAGTTCTGACAGCCAGTTGGGAAATAGCCTTAAGCAACATGCTTTGAGACACA	368
Oy	363	GGTCAAGTTCATTTGGCGTGAACCTTTCCTTCGATGACCTGTATATGCAAAAGAACAAAT	422
Db	369	ATCCACGTTTCATGAGATGAACCTTTCCTGTGATGACCTGTGATGGCGAAGAAAGACAAC	428
Oy	423	GGGCTGGGAAGCCGACACTGAGCGTTTGATCCCTCGATGAGCGGCTGTGAAGAAGAGAT	482
Db	429	TGTTTGGACCCATCTTTTGAAGAAATGACTGTCTGCGATGAAATATGAAAGGGGATGT	488
Oy	483	TCATTAAGGCTCTGAGCTGAAGAAAGACGGTGTCACTTACTAGTTGAATTCAAAAGTATTTA	542
Db	489	CACGCGTCTCTATGCTGCAAGGAGGTGGCAATTAAGATGCCAATTCACACATTTCTTA	548
Oy	543	CATGGCAAGAAGCCTGTGACGCTACCAAGGTACTAATGTGTACTCCAAACTGAGATAT	602
Db	549	CAAAACAAAAAACCGGGTGACGATGCCAACCAATGTGTGGAACAATCGCATTCGAG	608
Oy	603	AACAAGCCACAAGAGACTATACAATCGTTGACAGATAGA	644
Db	609	GACCGACCTTGACAAAGGTGCAACAGTGTTCACCTGACGA	650

```

RESULT 5
US-09-459-956-4
; Sequence 4, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, IIT, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REG01290-4
; CURRENT APPLICATION NUMBER: US/09/459, 956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765, 860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481, 977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 1 PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Zoanthus sp
US-09-459-956-4
;
Query Match      21.7%  Score 147.2;  DB 4;  Length 696;
Best Local Similarity 56.8%;  Pred. No. 1,1e-40;
Matches 316;  Conservative 0;  Mismatches 228;  Indels 12;  Gaps 2.;

```

Qy 9 TTCAAGAGTGTATCAAGAGCTTCAGAGGTTTAAGGTTGCGATGAGGAAGCAAGCTCA 68
Db 9 TTCAAGAGCGCTTAAAGAAATGACATGAAATACCAATGGAGGGTGCCTCA 68
Qy 69 TGGGCAAGAGTTTGAATAGAAAGGAGAGAGGGGACCATACGAAGGCCACATATAC 128
Db 69 CGGACATTAATTTTGATCAGGGGGAAGGCAATGGATATCCGTTCAAGGGGAAACAGAC 128
Qy 129 CGTAAGCTTAAGGTAAACCAAGGGGACCTTTGGCATTTTGGGATATTTTGTCAAC 188
Db 129 TATTATATTTGTGTGATCGAAGGGGACCATGTCATTTTCCGAAGCATATTTGTCAAC 188
Qy 189 ACAATTCAGTATGAGACCAAGATATATGCAAGCACCTGCCACATACCACTATTA 248
Db 189 TGGCTTAAATGACGAGACAGAGATTTTCACTGAATATCTCAAGACATATGATATTT 248
Qy 249 AAAGCTGATTTCTGTAAGATTTTAATGGGAAAGGCTGATGAACTTTGAAGCGG- 307
Db 249 CAAGAACTGTGTCTGCTGATATACATGGGGGCGCTTTTCTCTTGAAGATGGAGC 308
Qy 308 -----GCGTCTGTAAGTCAAGATTCAGATTCGAGATGGCTGTTTCACTCAAA 362
Db 309 AGTCTGATATGATGATATGATATACATGATGATCAAGAAACTGATTTATATTA 368
Qy 363 GGTCAAGTTCAATGGCGTGAACCTTCTTCCGATGACCTGTATGCAAAAGAACAT 422
Db 369 GAGCATATTTATGGAATGAATTTTCTGCTGATGACCTGTGATGAAAAAGATGACAC 428
Qy 423 GGGCTGGGAAGCCAGCACTGAGCGTT-----GATCTCTGTATGGCGTGTGAAG 476
Db 429 TAACCTGGAGACATCTGCGAGAGATCATGCGACGATCTTAAGCGGGGATATGAAAG 488
Qy 477 AGAGATTCATTAAGCTCTGAAGCTGAAGACGGTGTCTATTACCTAATTGAATCAAA 536
Db 489 GGATGTCTCCATGTACCTCTTCTGAAAGATGATGGGGGTTACCGGTGCAATGACAC 548
Qy 537 TATTTCATGGCAAG 552
Db 549 AGTTTACAAAGCAAG 564

RESULT 6
US-09-459-956-3
Sequence 3, Application US/0945956
Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US/09/459,956
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR FILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 696
TYPE: DNA
ORGANISM: Zoanthus sp
US-09-459-956-3

Query Match 19.7%; Score 133.4; DB 4; Length 696;
Best Local Similarity 55.3%; Pred. No. 6.3e-36;
Matches 307; Conservative 0; Mismatches 236; Indels 12; Gaps 2;
Qy 10 TCCAAGATGTATCAAGAGCTTCAGAGGTTTAAGGTTGCGATGAGGAAGCAAGCTCA 69
Db 10 TCCAAGATGTATCAAGAGCTTCAGAGGTTTAAGGTTGCGATGAGGAAGCAAGCTCA 69

Db 10 TCCAAGACCGCTTAAACAAAAGAAATGACATGAATACCGTATGGAAGGTCCTCGAT 69
Qy 70 GGGCAGCAGTTTGAATAGAAAGCGAAGAGAGGGAGGCCATACGAAGGCCAACATACC 129
Db 70 GGACATTAATTTTGATACAGGAGAGGGGCAATTGATATCTGTTCAAGGGAACAGGCT 129
Qy 130 GTAAAGCTTAAGGTAAACCAAGGGGACCTTTGCCATTTGCTTGGATATTTTGTACCA 189
Db 130 ATTATATGTGTGTGTGTCGAAGGTGACCATTCCTCAATTTGCCAAGACATATTTGTCA 189
Qy 190 CAATTCAGTATGGAAGCAAGATATATGCAAGCACCTTCGACATACCACTATTA 249
Db 190 GCCTTTACTACGAAACAGGGTTTTCATGAAATCTTCAAGACATATGATCTATTTTC 249
Qy 250 AAGCTGATTTCTGTAAGATTTAAATGGGAAAGGCTCATGAATTTGAAGACG---- 305
Db 250 AAGAACTCGTGTCTGTGTGATATACATGGGACAGGCTTTTCTCTTGAAGATGAGCA 309
Qy 306 --TGGCGTGTACTGTATACCCAGATTCAGATTTGCAAGATGGCTTTTCACTACAG 363
Db 310 GTTTCATATGATATGACATATATACAGTGAAGTTGMAAATCTGCATGTATCATAG 369
Qy 364 GTCAAGTTCAATGGCGTGAACCTTCTCCGATGACCTGTATGCAAAAGAACATAG 423
Db 370 TCCAATTTTATGAGATGAATTTTCTGCTGATGACCTGTGATGAAAAAGATGACAT 429
Qy 424 GGGCTGGAAACCAAGCACTGAGCGTT-----GATCTCTGTATGGCGTGTGAAGGA 477
Db 430 AACTGGAGCAATCTTCGAGAGATCATACAGTACTTAAGACAGGGGATATGAAAGGG 489
Qy 478 GAGATTCATTAAGCTCTGAAGCTGAAGACGGTGTCTATTACCTAATTGAATCAAAAG 537
Db 490 GATGTCTCAATGACCTCTTCTGAAGATGATGGGGGTTTACGGTCCAAATTCACACA 549
Qy 538 ATTACATGGCAAG 552
Db 550 GTTTTACAAAGCAAG 564

RESULT 7
US-09-609-161B-15
Sequence 15, Application US/09609161B
Patent No. 6436882
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: AND FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
FILE REFERENCE: 24729-121B
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 1079
TYPE: DNA
ORGANISM: Renilla mulleri
FEATURE:
NAME/KEY: CDS
LOCATION: (259)..(975)
OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-609-161B-15

Query Match 19.6%; Score 133.2; DB 4; Length 1079;
 Best Local Similarity 50.6%; Pred. No. 9,7e-36;
 Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

13 AGAATTTTCAAGAGTTTCAATGAGTTTAAAGTTGCAATGGAAGACGGTCAATGGG 72
 280 AACCTTTTCAAGAGTTTCAATGAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG 339
 73 CACGAGTTTAAATAGAGGCGAAGAGAGAGGAGGCGCATACGAAGCCCAATACCGTA 132
 340 CATGTTTTCATAGAGGAGTTGCGCAAGGAAATTTTATTCGGCAATCACTGGTT 399
 133 AAGCTTAAGTAAACAGAGGAGGAGCTTTGCGCATTTGCGGATATTTTGTCAACCA 192
 400 CAGATTGCTGTCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 459
 193 TTTCAGTATGGAAGCAAGGATATATGTCAGAGACCTGCGCATACGATCAATTAAG 252
 460 TTTCATATGAGCAAGGATATATGTCAGAGACCTGCGCATACGATCAATTAAG 519
 253 CTGTCAATTTCTGAAAGATTTAAATGGAAGAGGTCATGAACTTTGAAAGCGTGGC 312
 520 CAATCAATTTCCAGAGAGATTTATGATGAGAGAAATTAAGTTAGGATGAGGAGCT 579
 313 GTTACTGTAAACCAAGATTTCAATGTCAGAGATGCTTTTCACTTCAAGGTCAGTTC 372
 580 GTTGAATTCGTTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 639
 373 ATTGGCGTGAACCTTCTCCGATGAGCCTGTTATGAAAGAAAGCAATGAGGCTGG 432
 640 AAAGTATGTAATCTTCCAGATGATGTCCTGTCATGCAAGAGATCTTATGAGATGAG 699
 433 GCCAGACGAGCGTTTGTATCTCTGATGAGCGCTGTTGAAAGAGAGATTTAAGCT 492
 700 CTTTCAATTTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
 493 CTGAAGCTGAAGAGCGGTGCTCATTCCTTGTGATGATGATGATGATGATGATGAT 552
 760 TATTAACCTAACTCTGGAATATATTAATGTCATGCAATGAAACATTAATGAAGT 819
 553 AAGCGTGTGAGCTACAGAGGATCTATGTTGATGATGATGATGATGATGATGATGAT 612
 820 GGTGATGTAAGAGGATTTCTCTGATCAATTTTATTCACATGCTTTGAAAGACTTAC 879

613 AACGAAGCTATACATCGTTGAGCAGTATGAAA 646
 880 GTAGAAGACGGGGGCTTCGTTGAACAGCATGAGA 913

RESULT 8
 US-09-626-581D-64
 ; Sequence 64, Application US/09626581D
 ; Patent No. 6548249
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David
 ; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
 ; FILE REFERENCE: A-66900-3/RMS
 ; CURRENT APPLICATION NUMBER: US/09/626,581D
 ; CURRENT FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: 09/169,015
 ; PRIOR FILING DATE: 1998-10-08
 ; PRIOR APPLICATION NUMBER: 09/445,765
 ; PRIOR FILING DATE: 1999-10-08
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 64
 ; LENGTH: 1079
 ; TYPE: DNA
 ; ORGANISM: Renilla muelleri
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (259)..(975)

OTHER INFORMATION:
 US-09-626-581D-64

Query Match 19.6%; Score 133.2; DB 4; Length 1079;
 Best Local Similarity 50.6%; Pred. No. 9,7e-36;
 Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

13 AGAATTTTCAAGAGTTTCAATGAGTTTAAAGTTGCAATGGAAGACGGTCAATGGG 72
 280 AACCTTTTCAAGAGTTTCAATGAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAG 339
 73 CACGAGTTTAAATAGAGGCGAAGAGAGAGGAGGCGCATACGAAGCCCAATACCGTA 132
 340 CATGTTTTCATAGAGGAGTTGCGCAAGGAAATTTTATTCGGCAATCACTGGTT 399
 133 AAGCTTAAGTAAACAGAGGAGGAGCTTTGCGCATTTGCGGATATTTTGTCAACCA 192
 400 CAGATTGCTGTCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 459
 193 TTTCAGTATGGAAGCAAGGATATATGTCAGAGACCTGCGCATACGATCAATTAAG 252
 460 TTTCATATGAGCAAGGATATATGTCAGAGACCTGCGCATACGATCAATTAAG 519
 253 CTGTCAATTTCTGAAAGATTTAAATGGAAGAGGTCATGAACTTTGAAAGCGTGGC 312
 520 CAATCAATTTCCAGAGAGATTTATGATGAGAGAAATTAAGTTAGGATGAGGAGCT 579
 313 GTTACTGTAAACCAAGATTTCAATGTCAGAGATGCTTTTCACTTCAAGGTCAGTTC 372
 580 GTTGAATTCGTTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 639
 373 ATTGGCGTGAACCTTCTCCGATGAGCCTGTTATGAAAGAAAGCAATGAGGCTGG 432
 640 AAAGTATGTAATCTTCCAGATGATGTCCTGTCATGCAAGAGATCTTATGAGATGAG 699
 433 GCCAGACGAGCGTTTGTATCTCTGATGAGCGCTGTTGAAAGAGAGATTTAAGCT 492
 700 CTTTCAATTTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
 493 CTGAAGCTGAAGAGCGGTGCTCATTCCTTGTGATGATGATGATGATGATGATGATGAT 552
 760 TATTAACCTAACTCTGGAATATATTAATGTCATGCAATGAAACATTAATGAAGT 819
 553 AAGCGTGTGAGCTACAGAGGATCTATGTTGATGATGATGATGATGATGATGATGATGAT 612
 820 GGTGATGTAAGAGGATTTCTCTGATCAATTTTATTCACATGCTTTGAAAGACTTAC 879

613 AACGAAGCTATACATCGTTGAGCAGTATGAAA 646
 880 GTAGAAGACGGGGGCTTCGTTGAACAGCATGAGA 913

RESULT 9
 US-09-615-765B-64
 ; Sequence 64, Application US/09415765B
 ; Patent No. 6548632
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David
 ; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
 ; FILE REFERENCE: A66900-1/RMS/AMS
 ; CURRENT APPLICATION NUMBER: US/09/415,765B
 ; CURRENT FILING DATE: 1999-10-08
 ; PRIOR APPLICATION NUMBER: 09/169,015
 ; PRIOR FILING DATE: 1998-10-08
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ ID NO 64
 ; LENGTH: 1079
 ; TYPE: DNA
 ; ORGANISM: Renilla muelleri
 ; FEATURE:
 ; NAME/KEY: CDS

LOCATION: (259)..(975)
OTHER INFORMATION:
US-09-415-765B-64

Query Match 19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

```
QY 13 AAGAATGTTATCAAGAGTTCATGAGTTTAAAGTTCCCATGAAAGAACCGTCATGGG 72
DB 280 AACCTGTTTACAAAGAGTATGTCATATAAGTAATCTGGAAGAAATGTAACAC 339
QY 73 CACGAGTTTGAATTAAGAGCGAAGAGAGAGGAGGAGCCATACGAAGCCCAATACGCTA 132
DB 340 CATGTTTATCAAGAGAGGTTGCGCAAGGAAATATTTATTCGGCAATCACTGCT 399
QY 133 AAGCTTAAGTAAACCAAGGGGAGACCTTGGCATTTGCGGATATTTTGTCAACCA 192
DB 400 CAGATTGCTGTCAGAAAGGAGGCCCTGCTTTTGCATTTGATATTTGTCAACGCT 459
QY 193 TTTGATGAGAGCAAGATATATGTCAAGCACCTGCGCAATACCACTATPAAAA 252
DB 460 TTTGATATGAGAACCGTACTTTCAGAAATATCCGAATGATATATGATTTATTA 519
QY 253 CTGTCATTTCTGAAGATTTAATGGAAAGGTCATGAACCTTGAAGACGTCGCTC 312
DB 520 CAATCATTTTCCAGCAGATTTATGTATGACGAACATTACGTTACGAAGATGCGGACTT 579
QY 313 GTTACTGTAAACCAAGATTTCAAGTTGAGAGTGGCTTTTCATCTACAAGTCAAGTTC 372
DB 580 GTTGAATTCGTTCAAGATATTAATTTAATGAGCAAGTTGCTTACAGATGGAATAC 639
QY 373 ATTGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAAACAATGGCTGGAA 432
DB 640 AAAGTATGTAATCTCCAGATGATGTCCTCCGTCAGAGAAAGCATATTTGAATGAG 699
QY 433 GCCAGCACTGAGCGTTTGTATCTCGTATGAGCGCTGTGAAGAGAGATTCATAGGCT 492
DB 700 CTTTCATTTTGAAGCCATGTATGATGAATATGCGCTTGTGCGGAGATATTCCTGTC 759
QY 493 CTGAAGCTGAAGAGCGGTGTCATTAAGTGAATTCAAAGATTTATACAGGCAAG 552
DB 760 TATTAATCTAACTCGGGAATATTTATTCATGTCAATGAAACCTTAATAGTCGAA 819
QY 553 AAGCTGTGACACTACAGGCTACTATATGTGATCTCAACATGGAATATTAACAGCCAC 612
DB 820 GGTGATGAAGAGAGTTTCTTCGTATCATTTTATTAACAACCTTGAAGAAAGCTTAC 879
QY 613 AACGAAGCTATACATGCTTGAAGCATATGAAA 646
DB 880 GTAGAAAGCGGGGGTTCGTTGAACAGCATGAGA 913
```

RESULT 10
US-09-626-580C-64
Sequence 64, Application US/09626580C
Patent No. 6562617
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: FUSIONS OF SCAPFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES
FILE REFERENCE: A-66900-2/RMS/AAS
CURRENT APPLICATION NUMBER: US/09/626,580C
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 1079

TYPE: DNA
ORGANISM: Remilla muelleri
FEATURE:
NAME/KEY: CDS
LOCATION: (259)..(975)
OTHER INFORMATION:
US-09-626-580C-64

Query Match 19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

```
QY 13 AAGAATGTTATCAAGAGTTCATGAGTTTAAAGTTCCCATGAAAGAACCGTCATGGG 72
DB 280 AACCTGTTTACAAAGAGTATGTCATATAAGTAATCTGGAAGAAATGTAACAC 339
QY 73 CACGAGTTTGAATTAAGAGCGAAGAGAGAGGAGGAGCCATACGAAGCCCAATACGCTA 132
DB 340 CATGTTTATCAAGAGAGGTTGCGCAAGGAAATATTTATTCGGCAATCACTGCT 399
QY 133 AAGCTTAAGTAAACCAAGGGGAGACCTTGGCATTTGCGGATATTTTGTCAACCA 192
DB 400 CAGATTGCTGTCAGAAAGGAGGCCCTGCTTTTGCATTTGATATTTGTCAACGCT 459
QY 193 TTTGATGAGAGCAAGATATATGTCAAGCACCTGCGCAATACCACTATPAAAA 252
DB 460 TTTCAATATGGAACCGTACTTTCAGAAATATCCGAATGATATATGATTTATTA 519
QY 253 CTGTCATTTCTGAAGATTTAATGGAAAGGTCATGAACCTTGAAGACGTCGCTC 312
DB 520 CAATCATTTTCCAGCAGATTTATGTATGACGAACATTACGTTACGAAGATGCGGACTT 579
QY 313 GTTACTGTAAACCAAGATTTCAAGTTGAGAGTGGCTTTTCATCTACAAGTCAAGTTC 372
DB 580 GTTGAATTCGTTCAAGATATTAATTTAATGAGCAAGTTGCTTACAGATGGAATAC 639
QY 373 ATTGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAAACAATGGCTGGAA 432
DB 640 AAAGTATGTAATCTCCAGATGATGTCCTCCGTCAGAGAAAGCATATTTGAATGAG 699
QY 433 GCCAGCACTGAGCGTTTGTATCTCGTATGAGCGCTGTGAAGAGAGATTCATAGGCT 492
DB 700 CTTTCATTTTGAAGCCATGTATGATGAATATGCGCTTGTGCGGAGATATTCCTGTC 759
QY 493 CTGAAGCTGAAGAGCGGTGTCATTAAGTGAATTCAAAGATTTATACAGGCAAG 552
DB 760 TATTAATCTAACTCGGGAATATTTATTCATGTCAATGAAACCTTAATAGTCGAA 819
QY 553 AAGCTGTGACACTACAGGCTACTATATGTGATCTCAACATGGAATATTAACAGCCAC 612
DB 820 GGTGATGAAGAGAGTTTCTTCGTATCATTTTATTAACAACCTTGAAGAAAGCTTAC 879
QY 613 AACGAAGCTATACATGCTTGAAGCATATGAAA 646
DB 880 GTAGAAAGCGGGGGTTCGTTGAACAGCATGAGA 913
```

RESULT 11
US-09-277-716-15
Sequence 15, Application US/09277716A
Patent No. 6232107
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/079,624

EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1079
TYPE: DNA
ORGANISM: Renilla mulleri
FEATURE:
NAME/KEY: CDS
LOCATION: (259)..
FEATURE:
OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-277-716-15

Query Match 19.6%; Score 133.2; DB 3; Length 1085;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 13 AAGATGTTATCAAGAGTTTCATGAGTTTAAAGTTGCATGAGAGAACGGTCAATGGG 72
DB 280 AACACTGTTTACAAAGAGTATGTCGTATTAAGTAAATCTGGAAAGAAATGTTAAACAC 339
QY 73 CACAGTTTAAATAGAGGCGAAGAGAGGGGCGCATACAGAGCCCAATACGGTA 132
DB 340 CATGTTTTCACATAGAGGGGTGCGCAAGGGAAATTTTATTCCGCAATCACTGGTT 399
QY 133 AAGCTTAAGTTAACCAAGGGGGACCTTGGCATTTGCGATATTTTGTCAACCA 192
DB 400 CAGATTGTTGTCAGAAAGGGGGCCCACTGCTTTTGCATTTGATATTTGTCTACAGCT 459
QY 193 TTTTCAGTATGAGCAAGATATATGTCAGACCCCTGCGCATACAGACTATATAAAG 252
DB 460 TTTCAATATGCGCAACCTTACTTTCACGAAATATCCGATATATATCAATTTTATA 519
QY 253 CTGTCATTTCTGAGAGATTTAAATGGAAAGGTCATGAACTTGAAGCGGTGGGCTC 312
DB 520 CAATCATTTTCCAGAGATTTATGATATGAAACAACTTACGTTACGAAGATGGGCACTT 579
QY 313 GTTACTGTAAACCCAGATTCAGATTCAGAGATGGCTGTTTCATCTCAAGATCAAGTTTC 372
DB 580 GTTGAATTTGCTTCAATATTAATTTAATGAAACAAAGTTTCTGTCAGAGTGAATAC 639
QY 373 ATTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAACAAATGGCTGGAA 432
DB 640 AAGGTATGTAATCCAGATGATGTCCTGTCATGAGAAAGATATCTTGAAGATAGAG 699
QY 433 GCGCAGCACTAGACCTTTGATCCTCGATAGCGCTGTGAAGAGAGATTCATAAGGCT 492
DB 700 CTTTCATTTTGAAGCCATGATCATGAATTAATGGCGTCTTGGCGAAGTAAATCTTGTG 759
QY 493 CTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTTCAAAAGTATTTTACATGGCAAG 552
DB 760 TATTAATCTAAACTCTGGAAATATTTATTCATGTCATGAAAGAAATTAATGAAGTCCAAA 819
QY 553 AAGCTGTGACGTTACCAAGGTTACTATGTTGATCTCAAACTGATATTAACAAGCCAC 612
DB 820 GGTGTAGTAAAGAGATTCTCTTCTATCATCTTTTATTCAAACATGTTGAAAAAGACTTAC 879
QY 613 AACGAAGACTATACATCGTTGACAGTATGAAA 646
DB 880 GTAGAAAGACGGGGGTTGTTGAACAGCATGAGA 913

RESULT 12
US-09-277-716-30
Sequence 30, Application US/09277716A
Patent No. 6232107
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: US/09277,716A

CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 1104
TYPE: DNA
ORGANISM: Ptiliosarcus gunneyi
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..
FEATURE:
OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-277-716-30

Query Match 19.5%; Score 132.4; DB 3; Length 1104;
Best Local Similarity 50.3%; Pred. No. 1.9e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 13 AAGATGTTATCAAGAGTTTCATGAGTTTAAAGTTTCGATGAGAGAAACGGTCAATGGG 72
DB 55 AACACTGACTGAAGAGATTAATGTCGGCAAAAGCTAGCGTTGAAGAAATCGTAAACAT 114
QY 73 CACAGTTTAAATAGAGCGCAAGAGAGGGGCGCATACAGAGCCCAATACCGTA 132
DB 115 CACGTTTTCATGAGAGATTTGAAAAAGCGAATATTTATTTGAAAAACAAATGATG 174
QY 133 AAGCTTAAGTTAACCAAGGGGGACCTTGGCATTTTGGATATTTTGTCAACCA 192
DB 175 CAATCGGGTTTACAAAGGAGGTCCGTTGCCATTCGCTTTGATATTTGTTCCATAGCT 234
QY 193 TTTTCAGTATGAGCAAGATATATGTCAGACCCCTGCGCATACAGACTATATAAAG 252
DB 235 TTCCAATAGCGGAAATGCACTTTCACGAAATATCCAGAGCAATTCGCGCATCTTGT 294
QY 253 CTGTCATTTCTGAGAGATTTAAATGGAAAGGTCATGAACTTGAAGCGGTGGGCTC 312
DB 295 CAATCATTTCCGCGTGGATTTTCTACGAAAGAAATCTACGTTTGAAGATGGCGCAT 354
QY 313 GTTACTGTAAACCCAGATTCAGATTCAGAGATGGCTGTTTCATCTCAAGATCAAGTTTC 372
DB 355 GTTGAATTTGCTTCAATATTAATTTAATGAAAGATGATGTTCCATACAAAGTGAATAT 414
QY 373 ATTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAACCAATGGCTGGAA 432
DB 415 AGAGGCAACGGTTTCCCTGTAACGGAACCGTATCAAAAGCCCATCTCCGATAGAG 474
QY 433 GCGCAGCACTAGAGCTTTGATCCTCGATAGCGGTGTGAAGAGAGATTCATAAGGCT 492
DB 475 CACTGTTTGAAGGTGCTTACATGAACAGGGGTCTGTGGCGAAGTATCTCGTT 534
QY 493 CTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTTCAAAAGTATTTTACATGGCAAG 552
DB 535 TAAAGCTGAGTCAAGGAATATTTACTGTGCAATGAAACGTTTACATGCCAAA 594
QY 553 AAGCTGTGACGTTACCAAGGTTACTATGTTGATCTCAAACTGATATTAACAAGCCAC 612
DB 595 GGTGTAGTAAAGATTTCCCGAATATCACTTATCATCATCATGTCGTGAGAAACCTAC 654
QY 613 AACGAAGACTATACATCGTTGACAGTATGAAAAGAACCGAGGAC 658
DB 655 GTGAAAGAGAAAGCTTCTGTAACAAACAGAGCGCCATTTGCAC 700

RESULT 13
US-09-609-161B-30
Sequence 30, Application US/09609161B
Patent No. 643682

```

; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptiliosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-609-161B-30

```

```

Query Match      19.5%; Score 132.4; DB 4; Length 1104;
Best Local Similarity 50.3%; Pred. No. 1.9e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

```

```

Qy 13 AAGATGTTATCAAGAGTTCATGAGTTTAAGTTTCCATGGAAGCAAGCTCAATGG 72
Db 55 AACATGACTGAAGAAGATTATGTGCGCAAAAGCTAGCTGAAGAGATGTGAACAT 114
Qy 73 CACGAGTTTGAATATGAAGCGAAGAGAGAGGAGGAGCCATACGAAGCCACATACCTGA 132
Db 115 CACGTTTTCATGAGAGATTGGAAAAGGCAATGATATTGGAAGCAATATGATG 174
Qy 133 AAGCTTAAGTACCAAGAGGAGGAGCTTTGCCATTGCTTGAGATATTTTGTCAACCA 192
Db 175 CAATCCGCGTTTACAAAGAGAGTCCGTTGCCATTGCTTTCGATATGTTTCCATACCT 234
Qy 193 TTTGATGAGAGCAAGATATATGTCAAGCACCTGCGACATACGACATATATAAAG 252
Db 235 TTCCATATCGGGAATCGCACTTTCAGAAATACCAAGACGACATTCGGAATCTTTGTT 294
Qy 253 CTGTCAATTTCTGAAGATTATTAATGGAAAGGTCATGAATTTGAAGCGGTGGCTC 312
Db 295 CAATCATTTCCGGGCTGATTTTTCACGAAAGAAATCTACGTTTGAAGAGGGCCATT 354
Qy 313 GTTACTGTACCCAGAGATTCAGTTTGACAGATGGCTGTTTCACTTACAAAGTCAAGTTC 372
Db 355 GTTGACATTCGTTCAAGATATAGTTTAGAGATGATTAAGTTCCACTTCAAAAGTGAAT 414
Qy 373 ATTTGCGGGAATCTTCCGATGAGACCTGTTTATGCAAAAGAAAGCAATGGGCTGGAA 432
Db 415 AGAGCAACGCTTCCCTAGTACGAGCCCGTGAATGCAAAAGCCATCTCGGACATGAG 474
Qy 433 GCCAGCACTGAGCGTTTGTATCTCGATAGGCGGTGTGAAGAGAGATTCATTAAGCT 492
Db 475 CCATCGTTTGAAGTGTCTACATGAACAGCGCGCTTCGTGGGGAAGTATGATCGTT 534
Qy 493 CTGAAGCTGAAGAGCGTGTGATTAATCTAGTTGAATCAAAAGTATTTTACATGGCAAG 552
Db 535 TACAAACTCGAGTCAGGGAATATTAATCTGTCCACATGAAGAAACGTTTACAGATCCAA 594
Qy 553 AAGCGTGGAGCTCAAGGAGTACTATATGTTGACTCCAACTGGATATATCAAGGAC 612
Db 595 GGTGAGTGAAGAATTTCCCGGAATATCACTTATTCATCATCGTCTGAGAAACCTTAC 654

```

```

Qy 613 AACGAGACTATACATCTGTTGAGCACTATGAAGAAACGAGGAC 658
Db 655 GTGAGAGAGAAAGCTTGTGGAACAACACAGACGAGCCATTGGAC 700

```

```

RESULT 14
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Ptiliosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert B)
US-09-277-716-31

```

```

Query Match      19.5%; Score 132.4; DB 3; Length 1279;
Best Local Similarity 50.3%; Pred. No. 2e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

```

```

Qy 13 AAGATGTTATCAAGAGTTCATGAGTTTAAGTTTCCATGGAAGCAAGCTCAATGG 72
Db 28 AACCTGACTGAAGAAGATTATGTGCGCAAAAGCTAGCTGAAGAGATGTGAACAT 87
Qy 73 CACGAGTTTGAATATGAAGCGAAGAGAGAGGAGGAGCCATACGAAGCCACATACCTGA 132
Db 88 CACGTTTTCATGAGAGATTGGAAAAGGCAATGATATTGGAACCAATTTGATG 147
Qy 133 AAGCTTAAGTACCAAGAGGAGGAGCTTTGCCATTGCTTGAGATATTTTGTCAACCA 192
Db 148 CAATCCGCGTTTACAAAGAGAGTCCGTTGCCATTGCTTTCGATATGTTTCCATACCT 207
Qy 193 TTTGATGAGAGCAAGATATATGTCAAGCACCTGCGACATACGACATATATAAAG 252
Db 208 TTCCATATCGGGAATCGCACTTTCAGAAATACCAAGACGACATTCGGAATCTTTGTT 267
Qy 253 CTGTCAATTTCTGAAGATTATTAATGGAAAGGTCATGAATTTGAAGCGGTGGCTC 312
Db 268 CAATCATTTCCGGGCTGATTTTTCACGAAAGAAATCTACGCTTGAAGATGGGCCATT 327
Qy 313 GTTACTGTACCCAGAGATTCAGTTTGACAGATGGCTGTTTCACTTACAAAGTCAAGTTC 372
Db 328 GTTACATTCGTTCAAGATATAGTTTAGAGATGATTAAGTTCCATVCAAAAGTGAAT 387
Qy 373 ATTTGCGGGAATCTTCCGATGAGACCTGTTTATGCAAAAGAAAGCAATGGGCTGGAA 432
Db 388 AGAGCAACGCTTCCCTAGTACGAGCCCGTGAATGCAAAAGCCATCTCGGACATGAG 447
Qy 433 GCCAGCACTGAGCGTTTGTATCTCGATAGGCGGTGTGAAGAGAGATTCATTAAGCT 492
Db 448 CCATCGTTTGAAGTGTCTACATGAACAGCGCGCTTCGTGGGGAAGTATGATCTCGTT 507
Qy 493 CTGAAGCTGAAGAGCGGTGTGATTAATCTAGTTGAATTCAAAGATATTTTACATGGCAAG 552

```

Db 508 TACAACTCGAGTCAGGAACTATTACTCGTCCACATGAAAAGCTTTTACAGATCCAAA 567
Qy 553 AAGCTGTGAGCTACCAAGGAGTACTACTATGTTGACTCCAACTGATATTAACAAGCCAC 612
Db 568 GGTGAGATGAAGAATTCGCCGATATCACTTTATCCATCATCTCTCGAGAAAACCTAC 627
Qy 613 AACGAGACTATATACATCGTTGAGCAGTATGAAAAGAACCGAGGAC 658
Db 628 GTGAGAGAGAAAGCTTCGTGAAACAACGAGACGCGCATTTGCAC 673

RESULT 15
US-09-609-161B-31
; Sequence 31, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLOME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HI
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Ptiliosarcus guineyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert B)
; US-09-609-161B-31

Query Match 19.5%; Score 132.4; DB 4; Length 1279;
Best Local Similarity 50.3%; Pred. No. 2e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

Qy 13 AAGATGTATCAAGAGTTCATGAGTTTAAGGTTTGAAGGAGCAAGCGTCAATGGG 72
Db 28 AACCTGTGACTGAAGAAGATTATGTCGCAAAAGCTAGCGTGAAGAAATCGTGAACAAT 87
Qy 73 CACGAGTTTAATAGAAAGCGAAGAGAGGAGGCGCATACGAAGGCCCAATACCGTA 132
Db 88 CACGTTTTCATGAAAGATTGGAAGGCAATGATATTGGAACCAATGATG 147
Qy 133 AAGCTTAAGTAACCAAGGAGGAGCCTTTCGATTTGCGATATTTTGTCAACCAA 192
Db 148 CAATCCGGGTTACAAAGGAGGTCGTCGTCATTCGCTTTCGACATGTTTCCATAGCT 207
Qy 193 TTTCAGTATGAAGCAAGATATATGTCAAGCAACCTGCCGACATACCAAGATATAAAG 252
Db 208 TTCCAATACGGAATCGCACTTTCACGAATACCAAGACATGCGGACTACTTGT 267
Qy 253 CTGTCATTTCTGAAGATTTAAATGGAAGGGTCATGAACCTTGAAGACGTCGTC 312
Db 268 CAATCATTTCCGGCTGATTTTCTACGAAAGAAATCTACGCTTGAAGATGGCCAT 327
Qy 313 GTTACTGTAAACCGAGTTCAGTTTGAGATGCGTGTTCATCTCAAGGTCAAGTTC 372
Db 328 GTTGACATTCGTTCAATATTAAGTTTAGAAGATGATTAAGTTCCATCAAAAGTGAGAT 387

Qy 373 ATTGCGTGAACCTTCTTCCTCCATGAGACCTGTATATGCAAAAGAACATATGCGTGGAA 432
Db 388 AGAGGCAACGTTTCCCTAGTAAACGAGACCGGTGATCAAAAGCCATCCCTGCGCATGAG 447
Qy 433 GCCAGACTGAGCGTTTGTATCCTCGTATGCGGTGTAAGAGAGATTCATAAGGCT 492
Db 448 CCATCGTTTGAAGGTGCTTACATGAACAGCGGCTTGTGAGCGAAGTAGATCTCGTT 507
Qy 493 CTGAAGCTGAAGACCGGTGCTATTCATGTTGAATTCAAAAGTATTTACATGCGCAAG 552
Db 508 TACAACTCGAGTCAGGAACTATTACTGTGCAATGAAAACGTTTACGATCCAAA 567
Qy 553 AAGCTGTGAGCTACCAAGGATCTATGTTGACTCCAACTGATATTAACAAGCCAC 612
Db 568 GGTGAGATGAAGAATTCGCCGATATCACTTTATCCATCATCTCTCGAGAAAACCTAC 627
Qy 613 AACGAGACTATATACATCGTTGAGCAGTATGAAAAGAACCGAGGAC 658
Db 628 GTGAGAGAGAAAGCTTCGTGAAACAACGAGACGCGCATTTGCAC 673

Search completed: July 11, 2004, 11:16:48
Job time : 68 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2004, 09:54:11 ; Search time 50 Seconds
(without alignments)
1403.632 Million cell updates/sec

Title: US-10-006-922a-12
Perfect score: 1214
Sequence: 1 MESSKNVKEPMRKFVRMG.....EDTIVEQYRTRGRHFL 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgnt2_6/ptoddata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgnt2_6/ptoddata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgnt2_6/ptoddata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgnt2_6/ptoddata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgnt2_6/ptoddata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgnt2_6/ptoddata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgnt2_6/ptoddata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgnt2_6/ptoddata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgnt2_6/ptoddata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgnt2_6/ptoddata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgnt2_6/ptoddata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgnt2_6/ptoddata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgnt2_6/ptoddata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgnt2_6/ptoddata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgnt2_6/ptoddata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgnt2_6/ptoddata/2/pubpaa/US10C_NEW_PUB.pep:*
17: /cgnt2_6/ptoddata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgnt2_6/ptoddata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1214	100.0	225	9	US-09-999-745-67
2	1214	100.0	225	10	US-09-866-538-12
3	1214	100.0	225	10	US-09-794-308-12
4	1214	100.0	225	10	US-09-865-291-12
5	1214	100.0	225	12	US-10-132-067-4
6	1214	100.0	225	13	US-10-006-922-12
7	1214	100.0	225	14	US-10-081-864-8
8	1214	100.0	225	14	US-10-121-258-1
9	1214	100.0	225	14	US-10-315-920-2
10	1214	100.0	225	15	US-10-370-570-56
11	1214	100.0	225	15	US-10-406-618-32
12	1214	100.0	225	16	US-10-433-640-13
13	1214	100.0	487	15	US-10-343-977-1
14	1214	100.0	506	15	US-10-343-977-2
15	1214	100.0	547	15	US-10-343-977-3

16	1210	99.7	240	14	US-10-152-296-2	Sequence 2, Appli
17	1210	99.7	240	16	US-10-739-656-2	Sequence 2, Appli
18	1210	99.7	545	16	US-10-214-932-52	Sequence 52, Appli
19	1210	99.7	548	14	US-10-214-932-76	Sequence 76, Appli
20	1207	99.4	225	14	US-10-121-258-20	Sequence 20, Appli
21	1207	99.4	225	14	US-10-315-920-4	Sequence 4, Appli
22	1196	98.5	236	16	US-10-314-936-2	Sequence 2, Appli
23	1196	98.5	236	16	US-10-314-936-4	Sequence 4, Appli
24	1191	98.1	225	15	US-10-315-920-6	Sequence 6, Appli
25	1186	97.7	239	15	US-10-442-148A-7	Sequence 7, Appli
26	1186	97.7	239	15	US-10-442-148A-8	Sequence 8, Appli
27	1160	95.6	225	14	US-10-121-258-4	Sequence 4, Appli
28	1153	95.0	225	14	US-10-121-258-24	Sequence 24, Appli
29	1132	93.2	225	16	US-10-423-688A-41	Sequence 41, Appli
30	1121	92.3	226	14	US-10-121-258-6	Sequence 6, Appli
31	1119	92.2	225	13	US-10-006-922-44	Sequence 8, Appli
32	1119	92.2	225	14	US-10-081-864-12	Sequence 12, Appli
33	1085.5	89.4	230	13	US-10-006-922-18	Sequence 18, Appli
34	1085.5	89.4	230	14	US-10-161-403-40	Sequence 40, Appli
35	1046	86.2	205	13	US-10-006-922-46	Sequence 46, Appli
36	1021	84.1	225	14	US-10-121-258-8	Sequence 8, Appli
37	765	63.0	227	13	US-10-006-922-10	Sequence 10, Appli
38	729.5	60.1	232	14	US-10-133-973-5	Sequence 5, Appli
39	729.5	60.1	232	15	US-10-370-570-64	Sequence 64, Appli
40	690	56.8	225	15	US-10-370-570-61	Sequence 61, Appli
41	681	56.1	225	14	US-10-244-779-2	Sequence 2, Appli
42	680.5	56.1	227	14	US-10-314-827-4	Sequence 4, Appli
43	680.5	56.1	227	14	US-10-314-827-6	Sequence 6, Appli
44	680.5	56.1	227	14	US-10-314-827-8	Sequence 8, Appli
45	680.5	56.1	227	14	US-10-314-827-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-999-745-67
; Sequence 67, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 67
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-999-745-67

Query Match	100.0%	Score 1214;	DB 9;	Length 225;
Best Local Similarity	100.0%	Pred. No. 1,6e-120;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MESSKNVKEPMRKFVRMG	EVNHEFEIEGEGRPYEGHNTVKLKTGKGPLPRAWDI	60
DB	1	MESSKNVKEPMRKFVRMG	EVNHEFEIEGEGRPYEGHNTVKLKTGKGPLPRAWDI	60
QY	61	LSPOFGYGVKVVYKHPADIPDYKLSFPPGFKMERVMNEEDGVTYVODSSLQDCFTY	120	
DB	61	LSPOFGYGVKVVYKHPADIPDYKLSFPPGFKMERVMNEEDGVTYVODSSLQDCFTY	120	
QY	121	KYKFIQVNPSPDGPVWQKTKMGWEASTERTLYPRDGVTKGEIKHALKLDKDGHYIVFPKSI	180	
DB	121	KYKFIQVNPSPDGPVWQKTKMGWEASTERTLYPRDGVTKGEIKHALKLDKDGHYIVFPKSI	180	

Qy 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225
Db 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225

RESULT 2
US-09-866-538-12
; Sequence 12, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: *Dicosoma* sp.
US-09-866-538-12

Query Match 100.0%; Score 1214; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60
Db 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60

Qy 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120
Db 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120

Qy 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180
Db 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180

Qy 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225
Db 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225

RESULT 3
US-09-794-308-12
; Sequence 12, Application US/09794308
; Publication No. US20030170911A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, Roger
; APPLICANT: ZACHARIAS, David
; APPLICANT: BAIRD, Geoffrey
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530
; CURRENT APPLICATION NUMBER: US/09/794,308
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: *Dicosoma* sp.
US-09-794-308-12

Query Match 100.0%; Score 1214; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60
Db 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60

Db 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60
Qy 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120
Db 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120

Qy 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180
Db 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180

Qy 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225
Db 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225

RESULT 4
US-09-865-291-12
; Sequence 12, Application US/09865291
; Publication No. US20030186229A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEN, Roger
; APPLICANT: TING, Alice
; APPLICANT: ZHANG, Jin
; TITLE OF INVENTION: EMISSION RATIONETRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: REGEN1550
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: *Dicosoma* sp.
US-09-865-291-12

Query Match 100.0%; Score 1214; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60
Db 1 MRSSKNVYKEPFRFVYRMEGTVNGHFEIIEGEGRPYEGHNTVYKLTGKGPLPFAMD 60

Qy 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120
Db 61 LSPQFYGSKYVYKHPADIDPYKKLSPEGFKMERVWNFEDGVVTVTQDSSLQDGCFTY 120

Qy 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180
Db 121 KYKFIGVNPSPDGPVWQKTMGWEASTERLYPRDGVLKGEIHAKLKLKDGHYLVEFKSI 180

Qy 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225
Db 181 YMAKPPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTGRRHFL 225

RESULT 5
US-10-132-067-4
; Sequence 4, Application US/10132067
; Publication No. US20030203355A1
; GENERAL INFORMATION:
; APPLICANT: Bradbury, Andrew
; APPLICANT: Zeytun, Ahmet
; APPLICANT: Waldo, Geoffrey
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fluorobodies: Binding Ligands with Intrinsic
; FILE REFERENCE: 021362-000600US
; CURRENT APPLICATION NUMBER: US/10/132,067
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
; FEATURE:
; OTHER INFORMATION: red fluorescent protein (dared)
US-10-132-067-4

```

```

Query Match      100.0%; Score 1214; DB 12; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
DB 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
QY 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||
DB 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||
QY 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
DB 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
QY 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||
DB 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||

```

RESULT 6

```

US-10-006-922-12
; Sequence 12, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A.
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labae, Yulii A.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Tetsikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
; TITLE OF INVENTION: Method for Using the Same
; FILE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US/10/006,922
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma species
US-10-006-922-12

```

```

Query Match      100.0%; Score 1214; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
DB 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
QY 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||

```

```

DB 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||
QY 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
DB 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
QY 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||
DB 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||

```

RESULT 7

```

US-10-081-864-8
; Sequence 8, Application US/10081864
; Publication No. US2003002287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-081-864-8

```

```

Query Match      100.0%; Score 1214; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
DB 1 MRSSKNVKEFMFKRMESTVNGHEFEIEGEGRGREYEGHNTVKLTGKGPLPFAWMI 60
   |||
QY 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||
DB 61 LSPQFGYSKYVYKHPADIPDYKLSFPEGFKMERVMNFDGVTYTTODSSIQDGCFTY 120
   |||
QY 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
DB 121 KYAFIGNFSPDGPVWQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
   |||
QY 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||
DB 181 YMAKPVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
   |||

```

RESULT 8

```

US-10-121-258-1
; Sequence 1, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP1
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308

```

```

; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(225)
; OTHER INFORMATION: wild-type Dared
US-10-121-258-1

Query Match      100.0%; Score 1214; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
QY 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
DB 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
QY 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
DB 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 9
US-10-315-920-2
; Sequence 2, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315,920
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-315-920-2

Query Match      100.0%; Score 1214; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
QY 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
DB 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
QY 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
DB 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 10
US-10-370-570-56
; Sequence 56, Application US/10370570
; Publication No. US20030219717A1
; GENERAL INFORMATION:
; APPLICANT: DAHL, Soren Weis et al.
; TITLE OF INVENTION: FLUOROPHORE COMPLEMENTATION PRODUCTS
; FILE REFERENCE: 3759-0130P
; CURRENT APPLICATION NUMBER: US/10/370,570
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-370-570-56

Query Match      100.0%; Score 1214; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
QY 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
DB 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
QY 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
DB 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 11
US-10-406-618-32
; Sequence 32, Application US/10406618
; Publication No. US20030219814A1
; GENERAL INFORMATION:
; APPLICANT: Man, David Chi-Cheong
; APPLICANT: Ip, Denise Taz-Ming
; TITLE OF INVENTION: No. US20030219814A1 Fluorescent Proteins
; FILE REFERENCE: 016285-34-1
; CURRENT APPLICATION NUMBER: US/10/406,618
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/387,968
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/370,598
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Spontaneously
; OTHER INFORMATION: Fluorescent protein Dared.
US-10-406-618-32
```

```

|||||
DB 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 10
US-10-370-570-56
; Sequence 56, Application US/10370570
; Publication No. US20030219717A1
; GENERAL INFORMATION:
; APPLICANT: DAHL, Soren Weis et al.
; TITLE OF INVENTION: FLUOROPHORE COMPLEMENTATION PRODUCTS
; FILE REFERENCE: 3759-0130P
; CURRENT APPLICATION NUMBER: US/10/370,570
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-370-570-56

Query Match      100.0%; Score 1214; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVYKLVTKGGLPFPAMD 60
QY 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
DB 61 LSPQFQYGSKYVYKHADIPDYKLSFPEGFKMERVMNPFEDGVTVTQDSSLQDGCFTY 120
QY 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
DB 121 KYKFIGVNPSPDGPVMQKKTGMWEASTERLYPRDGVKGEIHKALKKDGGHYLVPEFSK 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 11
US-10-406-618-32
; Sequence 32, Application US/10406618
; Publication No. US20030219814A1
; GENERAL INFORMATION:
; APPLICANT: Man, David Chi-Cheong
; APPLICANT: Ip, Denise Taz-Ming
; TITLE OF INVENTION: No. US20030219814A1 Fluorescent Proteins
; FILE REFERENCE: 016285-34-1
; CURRENT APPLICATION NUMBER: US/10/406,618
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/387,968
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/370,598
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Spontaneously
; OTHER INFORMATION: Fluorescent protein Dared.
US-10-406-618-32
```


Query Match 100.0%; Score 1214; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
DB 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
QY 61 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 120
DB 61 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 120
QY 121 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 180
DB 121 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 225

RESULT 12

US-10-433-640-13
; Sequence 13, Application US/10433640
; Publication No. US20040115792A1
; GENERAL INFORMATION:
; APPLICANT: Liechtenberg-Faate, Hella
; TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
; TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS
; FILE REFERENCE: 1487/3
; CURRENT APPLICATION NUMBER: US/10/433, 640
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/14610
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: DE 10061872.3
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discoecoma sp.
US-10-433-640-13

Query Match 100.0%; Score 1214; DB 16; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
DB 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
QY 61 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 120
DB 61 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 120
QY 121 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 180
DB 121 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 225

RESULT 13

US-10-343-977-1
; Sequence 1, Application US/10343977
; Publication No. US20040014134A1
; GENERAL INFORMATION:
; APPLICANT: Kuhlmann, Rene
; APPLICANT: Koltermann, Andre

; APPLICANT: Ketting, Ulrich
; APPLICANT: Schwillie, Petra
; TITLE OF INVENTION: Dual Coloured Fluorimetric protease assay
; FILE REFERENCE: 023425us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/343, 977
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: PCT/EP01/09112
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Autofluorescent fusion protein derived from GFP variants of
; OTHER INFORMATION: e.g. Aequorea victoria and/or Discoecoma sp.

Query Match 100.0%; Score 1214; DB 15; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.9e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
DB 263 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 322
QY 61 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 120
DB 323 LSPFOYGSKYVYVGHADIDYKLSFPEGFKMERVMNPFEDGCVYVTTODSSLODGCFTY 382
QY 121 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 180
DB 383 KVFIFGVNPFSDGVMQKTMGWEASTERYLPYRDGVLKGEIHKALKDKGHYLVEFKSI 442
QY 181 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 225
DB 443 YMAKKPVQLPGYVYVDSKLDITSNEDYTVIVEOYERTEGRHHLFL 487

RESULT 14

US-10-343-977-2
; Sequence 2, Application US/10343977
; Publication No. US20040014134A1
; GENERAL INFORMATION:
; APPLICANT: Kuhlmann, Rene
; APPLICANT: Ketting, Ulrich
; APPLICANT: Schwillie, Petra
; TITLE OF INVENTION: Dual Coloured Fluorimetric protease assay
; FILE REFERENCE: 023425us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/343, 977
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: PCT/EP01/09112
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Autofluorescent fusion protein derived from GFP variants of
; OTHER INFORMATION: e.g. Aequorea victoria and/or Discoecoma sp.

Query Match 100.0%; Score 1214; DB 15; Length 506;
Best Local Similarity 100.0%; Pred. No. 5.2e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 60
DB 282 MRSSKNVKEFMFKRMGTGTVNGHEFEIEGEGRPYEGHNTVTKLVTYKGGPLPFAMDI 341

QY 61 LSPQFYSSKYYVVKHPADIPIYKKLSPEGFKMERVMNFDGGVVTYTQDSSLQDGCFTY 120
Db 342 LSPQFYSSKYYVVKHPADIPIYKKLSPEGFKMERVMNFDGGVVTYTQDSSLQDGCFTY 401
QY 121 KVKFIGNVFPDSGPMQKKTGMWEASTERYLPDGVKGEIHKALKLKDGGHYLVEPKSI 180
Db 402 KVKFIGNVFPDSGPMQKKTGMWEASTERYLPDGVKGEIHKALKLKDGGHYLVEPKSI 461
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 462 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 506

RESULT 15

US-10-343-977-3
; Sequence 3, Application US/10343977
; Publication No. US20040014134A1
; GENERAL INFORMATION:
; APPLICANT: Kuhlmann, Rene
; APPLICANT: Koitlermann, Andre
; APPLICANT: Ketting, Ulrich
; APPLICANT: Schwillie, Petra
; TITLE OF INVENTION: Dual coloured fluorimetric protease assay
; FILE REFERENCE: 023425us/3H/ml
; CURRENT APPLICATION NUMBER: US/10/343,977
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: PCT/EP01/09112
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Autofluorescent fusion protein derived from GFP variants of
; OTHER INFORMATION: e.g. Aequorea victoria and/or Discosoma sp.
US-10-343-977-3

Query Match 100.0%; Score 1214; DB 15; Length 547;
Best local similarity 100.0%; Pred. No. 5.8e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFVMEGVNGHFEIEGEGRPYEGHNTYKLVKTKGAPLPFANDI 60
Db 323 MRSSKNVKEFMRFVMEGVNGHFEIEGEGRPYEGHNTYKLVKTKGAPLPFANDI 382
QY 61 LSPQFYSSKYYVVKHPADIPIYKKLSPEGFKMERVMNFDGGVVTYTQDSSLQDGCFTY 120
Db 383 LSPQFYSSKYYVVKHPADIPIYKKLSPEGFKMERVMNFDGGVVTYTQDSSLQDGCFTY 442
QY 121 KVKFIGNVFPDSGPMQKKTGMWEASTERYLPDGVKGEIHKALKLKDGGHYLVEPKSI 180
Db 443 KVKFIGNVFPDSGPMQKKTGMWEASTERYLPDGVKGEIHKALKLKDGGHYLVEPKSI 502
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 503 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 547

Search completed: July 8, 2004, 10:00:33
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 10:35:36 ; Search time 316 Seconds
(without alignments)
10457.256 Million cell updates/sec

Title: US-10-006-922a-11

Perfect score: 678
Sequence: 1 atgaggtcttccaagaatgc.....gccaccatctgtcctttaa 678

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq2:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	9	US-09-967-772-6
2	678	100.0	678	13	US-10-132-067-3
3	678	100.0	678	14	US-10-006-922-11
4	678	100.0	678	15	US-10-121-258-2
5	678	100.0	678	16	US-10-335-517-6
6	678	100.0	678	16	US-10-334-288-6
7	678	100.0	859	9	US-09-999-745-66
8	678	100.0	859	10	US-09-866-538-11
9	678	100.0	859	10	US-09-794-308-11
10	678	100.0	859	17	US-09-865-291-11
11	678	100.0	859	17	US-10-433-640-12
12	677	99.9	3311	10	US-09-797-4968-3
13	665	98.1	666	17	US-10-332-733-22
14	661	97.5	711	17	US-10-314-936-1

15	661	97.5	711	17	US-10-314-936-3	Sequence 3, Appl1
16	658.8	97.2	898	17	US-10-006-922-45	Sequence 45, Appl1
17	642.8	94.8	678	14	US-10-423-688A-40	Sequence 40, Appl1
18	566.4	83.5	876	14	US-10-006-922-17	Sequence 17, Appl1
19	566.4	83.5	876	15	US-10-161-403-39	Sequence 39, Appl1
20	450.6	66.5	723	15	US-10-152-296-1	Sequence 1, Appl1
21	450.6	66.5	723	17	US-10-739-666-1	Sequence 1, Appl1
22	449.2	66.3	678	15	US-10-081-864-7	Sequence 7, Appl1
23	449.2	66.3	678	15	US-10-315-920-1	Sequence 1, Appl1
24	447.2	66.0	681	15	US-10-121-258-3	Sequence 3, Appl1
25	447.2	66.0	681	15	US-10-121-258-23	Sequence 23, Appl1
26	447.2	66.0	4692	15	US-10-161-403-29	Sequence 29, Appl1
27	447.2	66.0	4692	17	US-10-433-640-16	Sequence 16, Appl1
28	447.2	66.0	6984	17	US-10-001-188-45	Sequence 45, Appl1
29	446	65.8	678	15	US-10-315-920-3	Sequence 3, Appl1
30	445.8	65.8	1638	15	US-10-214-932-51	Sequence 51, Appl1
31	445.8	65.8	1647	15	US-10-214-932-75	Sequence 75, Appl1
32	445.6	65.7	681	14	US-10-006-922-35	Sequence 35, Appl1
33	440.8	65.0	681	14	US-10-006-922-37	Sequence 37, Appl1
34	439.6	64.8	678	15	US-10-315-920-5	Sequence 5, Appl1
35	438	64.6	678	14	US-10-006-922-36	Sequence 36, Appl1
36	438	64.6	678	15	US-10-081-864-14	Sequence 14, Appl1
37	437	64.5	1050	14	US-10-060-857-7	Sequence 38, Appl1
38	435.6	64.2	675	15	US-10-081-864-13	Sequence 13, Appl1
39	435.6	64.2	675	15	US-10-006-922-9	Sequence 9, Appl1
40	434.6	64.1	850	14	US-10-121-258-5	Sequence 5, Appl1
41	432.2	63.7	678	15	US-10-121-258-7	Sequence 7, Appl1
42	410.4	60.5	681	9	US-09-967-772-5	Sequence 5, Appl1
43	409.6	60.4	699	15	US-10-335-517-5	Sequence 5, Appl1
44	409.6	60.4	699	16	US-10-334-288-5	Sequence 5, Appl1
45	409.6	60.4	699	16	US-10-334-288-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-967-772-6
Sequence 6, Application US/09967772
Patent No. US20020164577A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSJEN, Roger
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
FILE REFERENCE: REGEN1290-5
CURRENT APPLICATION NUMBER: US/09/967,772
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: US 08/481,977
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 678
TYPE: DNA
ORGANISM: Discoosoma sp "red"
US-09-967-772-6

Query Match 100.0%; Score 678; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.2e-216; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

QY 1 ATGAGTCTTCCAGAGATGTTATCAAGAGTTCATGAGGTTTAAGGTTGATGAAGA 60
DB 1 ATGAGTCTTCCAGAGATGTTATCAAGAGTTCATGAGGTTTAAGGTTGATGAAGA 60
QY 61 ACGGTCAATGGACGAGGTTTGAATATGAAGGCAAGAGAGAGGCCATATGCAAGGC 120

```
|||||
Db 61 ACGGTCATGGGCGACGAGTTTGAATAGAACGCGAGGAGGAGGAGGCGATACGAAAGGC 120
Qy 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGGCAATTTGCTTGGGATATT 180
Db 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGGCAATTTGCTTGGGATATT 180
Qy 181 TTGTCAACCAATTTCAAGTATGAAAGCAAGGTATATGTCAAGCAACCTTCCGACATACCA 240
Db 181 TTGTCAACCAATTTCAAGTATGAAAGCAAGGTATATGTCAAGCAACCTTCCGACATACCA 240
Qy 241 GACTATATAAAGCTGTCTATTTCTTGAAGAGATTAAATGGGAAAGGTTCATACCTTTGAA 300
Db 241 GACTATATAAAGCTGTCTATTTCTTGAAGAGATTAAATGGGAAAGGTTCATACCTTTGAA 300
Qy 301 GACGGTGGCGTCTGTACTGTAAACCAAGGATTCAGATTTCAGAGATGGCTGTTTCATCTAC 360
Db 301 GACGGTGGCGTCTGTACTGTAAACCAAGGATTCAGATTTCAGAGATGGCTGTTTCATCTAC 360
Qy 361 AAGGTCAAGTTCAATTGGCGTGAATCTTTCCTTCGATGACCTGTTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCAATTGGCGTGAATCTTTCCTTCGATGACCTGTTATGCAAAAGAGACA 420
Qy 421 ATGGGCTGGGAAGCCAGACCTGAGGTTGTATCCTCGTGAATGGCGTTTGAAGAGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGACCTGAGGTTGTATCCTCGTGAATGGCGTTTGAAGAGAGAG 480
Qy 481 ATTCAATAAGGCTCTGACACTGAAAGACGAGGTTGATCCTGTAATGGCGTTTGAAGAGAG 540
Db 481 ATTCAATAAGGCTCTGACACTGAAAGACGAGGTTGATCCTGTAATGGCGTTTGAAGAGAT 540
Qy 541 TACATGGCAAAAGAAAGCTGTGACGCTACCAAGGTAATCTATGTTGACTCCAAACTGAT 600
Db 541 TACATGGCAAAAGAAAGCTGTGACGCTACCAAGGTAATCTATGTTGACTCCAAACTGAT 600
Qy 601 ATAAACAGCCCAAGAGAGACTATCATCGTTGAGCATGTAAGAAAGACGAGGAGAGC 660
Db 601 ATAAACAGCCCAAGAGAGACTATCATCGTTGAGCATGTAAGAAAGACGAGGAGAGC 660
Qy 661 CACCATCTGTTCTTTAA 678
Db 661 CACCATCTGTTCTTTAA 678

RESULT 2
US-10-132-067-3
; Sequence 3, Application US//10132067
; Publication No. US20030203355A1
; GENERAL INFORMATION:
; APPLICANT: Bradbury, Andrew
; APPLICANT: Zeytun, Ahmet
; APPLICANT: Waldo, Geoffrey
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fluorobodies: Binding Ligands With Intrinsic
; TITLE OF INVENTION: Fluorescence
; FILE REFERENCE: 021362-000600US
; CURRENT APPLICATION NUMBER: US/10/132,067
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; OTHER INFORMATION: red fluorescent protein (dsRed)
; NAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: dsRed
US-10-132-067-3
Query Match 100.0%; Score 678; DB 13; Length 678;
```

```
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
|||||
Qy 1 ATAGAGCTTTCGAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTGCGATGAAAGA 60
Db 1 ATAGAGCTTTCGAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTGCGATGAAAGA 60
Qy 61 ACGGTCAATGGGCAAGATTGAAATATGAAAGCGGAAAGAGAGGAGCCATACGAAGGC 120
Db 61 ACGGTCAATGGGCAAGATTGAAATATGAAAGCGGAAAGAGAGGAGCCATACGAAGGC 120
Qy 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGGCAATTTGCTTGGGATATT 180
Db 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGGCAATTTGCTTGGGATATT 180
Qy 181 TTGTCAACCAATTTCAAGTATGAAAGCAAGGTATATGTCAAGCAACCTTCCGACATACCA 240
Db 181 TTGTCAACCAATTTCAAGTATGAAAGCAAGGTATATGTCAAGCAACCTTCCGACATACCA 240
Qy 241 GACTATATAAAGCTGTCTATTTCTTGAAGAGATTAAATGGGAAAGGTTCATACCTTTGAA 300
Db 241 GACTATATAAAGCTGTCTATTTCTTGAAGAGATTAAATGGGAAAGGTTCATACCTTTGAA 300
Qy 301 GACGGTGGCGTCTGTACTGTAAACCAAGGATTCAGATTTCAGAGATGGCTGTTTCATCTAC 360
Db 301 GACGGTGGCGTCTGTACTGTAAACCAAGGATTCAGATTTCAGAGATGGCTGTTTCATCTAC 360
Qy 361 AAGGTCAAGTTCAATTGGCGTGAATCTTTCCTTCGATGACCTGTTATGCAAAAGAGACA 420
Db 361 AAGGTCAAGTTCAATTGGCGTGAATCTTTCCTTCGATGACCTGTTATGCAAAAGAGACA 420
Qy 421 ATGGGCTGGGAAGCCAGACCTGAGGTTGTATCCTCGTGAATGGCGTTTGAAGAGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGACCTGAGGTTGTATCCTCGTGAATGGCGTTTGAAGAGAGAG 480
Qy 481 ATTCAATAAGGCTCTGACACTGAAAGACGAGGTTGATCCTGTAATGGCGTTTGAAGAGAT 540
Db 481 ATTCAATAAGGCTCTGACACTGAAAGACGAGGTTGATCCTGTAATGGCGTTTGAAGAGAT 540
Qy 541 TACATGGCAAAAGAAAGCTGTGACGCTACCAAGGTAATCTATGTTGACTCCAAACTGAT 600
Db 541 TACATGGCAAAAGAAAGCTGTGACGCTACCAAGGTAATCTATGTTGACTCCAAACTGAT 600
Qy 601 ATAAACAGCCCAAGAGAGACTATCATCGTTGAGCATGTAAGAAAGACGAGGAGAGC 660
Db 601 ATAAACAGCCCAAGAGAGACTATCATCGTTGAGCATGTAAGAAAGACGAGGAGAGC 660
Qy 661 CACCATCTGTTCTTTAA 678
Db 661 CACCATCTGTTCTTTAA 678

RESULT 3
US-10-006-922-11
; Sequence 11, Application US//10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yulii A.
; APPLICANT: Metz, Mikhail V.
; APPLICANT: Tetsikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US//10/006,922
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
```

```

; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Dicosoma species
US-10-006-922-11

```

```

Query Match      100.0%; Score 678; DB 14; Length 678;
Best Local Similarity 100.0%; Pred.No.1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATGAGGCTCTCCAGAAATGTTATCAAGAGTTCAATGAGTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGGCTCTCCAGAAATGTTATCAAGAGTTCAATGAGTTAAAGTTCCGATGGAAGA 60
QY 61 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAGAGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAGAGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CACAATACCGTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CACAATACCGTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 TTGTCAACCAATTTCAATGAGAGAGGATATATGTCAAGCAGCCTGCGGACATACCA 240
DB 181 TTGTCAACCAATTTCAATGAGAGAGGATATATGTCAAGCAGCCTGCGGACATACCA 240
QY 241 GACTATTAAGGCTGATATTCGAGAGAGTTTAAATGAGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 GACTATTAAGGCTGATATTCGAGAGAGTTTAAATGAGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 GAGGTCGCGTCTGTTACTGTAAACCAAGATTCAGATTGAGAGATGAGCTGTTTCACTAC 360
DB 301 GAGGTCGCGTCTGTTACTGTAAACCAAGATTCAGATTGAGAGATGAGCTGTTTCACTAC 360
QY 361 AAGGTCAGTTCAATGGCGTGAATCTTCTCCGATGAGCCTGTTATGCAAAAGAGACA 420
DB 361 AAGGTCAGTTCAATGGCGTGAATCTTCTCCGATGAGCCTGTTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAGAGCGACGACCTGAGCGTTGATCTGATAGCGGCTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAGAGCGACGACCTGAGCGTTGATCTGATAGCGGCTGTTGAAAGAGAG 480
QY 481 ATTCAATAGGCTGTAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTCAATAGGCTGTAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TACATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 TACATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ATAAACAAGCACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 ATAAACAAGCACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

```

```

RESULT 4
US-10-121-258-2
; Sequence 2, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger

```

```

; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; FILE REFERENCE: UC083.1CP2CP1
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Dicosoma sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type DsRed
US-10-121-258-2

```

```

Query Match      100.0%; Score 678; DB 15; Length 678;
Best Local Similarity 100.0%; Pred.No.1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATGAGGCTCTCCAGAAATGTTATCAAGAGTTCAATGAGTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGGCTCTCCAGAAATGTTATCAAGAGTTCAATGAGTTAAAGTTCCGATGGAAGA 60
QY 61 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAGAGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAGAGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CACAATACCGTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CACAATACCGTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 TTGTCAACCAATTTCAATGAGAGAGGATATATGTCAAGCAGCCTGCGGACATACCA 240
DB 181 TTGTCAACCAATTTCAATGAGAGAGGATATATGTCAAGCAGCCTGCGGACATACCA 240
QY 241 GACTATTAAGGCTGATATTCGAGAGAGTTTAAATGAGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 GACTATTAAGGCTGATATTCGAGAGAGTTTAAATGAGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 GAGGTCGCGTCTGTTACTGTAAACCAAGATTCAGATTGAGAGATGAGCTGTTTCACTAC 360
DB 301 GAGGTCGCGTCTGTTACTGTAAACCAAGATTCAGATTGAGAGATGAGCTGTTTCACTAC 360
QY 361 AAGGTCAGTTCAATGGCGTGAATCTTCTCCGATGAGCCTGTTATGCAAAAGAGACA 420
DB 361 AAGGTCAGTTCAATGGCGTGAATCTTCTCCGATGAGCCTGTTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAGAGCGACGACCTGAGCGTTGATCTGATAGCGGCTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAGAGCGACGACCTGAGCGTTGATCTGATAGCGGCTGTTGAAAGAGAG 480
QY 481 ATTCAATAGGCTGTAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTCAATAGGCTGTAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TACATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 TACATGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ATAAACAAGCACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 ATAAACAAGCACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

```

```
RESULT 5
US-10-335-517-6
; Sequence 6, Application US/10335517
; Publication No. US20030207248A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: GONZALEZ, Jesus
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
; FILE REFERENCE: REGEN1290-5
; CURRENT APPLICATION NUMBER: US/10/335,517
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/967,772
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 08/765,860
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/ US96/09652
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/481,977
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp "red"
US-10-335-517-6
```

```
Query Match      100.0%; Score 678; DB 16; Length 678;
Best Local Similarity 100.0%; Pred. No. 1,2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGAGCTTCCAGAAATGTTATCAAGAGTTTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTTCATGAGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACGGTCATGCGGACAGAGTTTGAATAGAGCGAAGGAGAGGAGGCGCATACGAAGGC 120
DB 61 ACGGTCATGCGGACAGAGTTTGAATAGAGCGAAGGAGAGGAGGCGCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
QY 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
QY 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
DB 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
QY 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
DB 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
QY 241 GACTATATAAAGCTGTCAATTTCTGAAGATTTTAAATGGAAAGGGTCATGAACCTTTGAA 300
DB 241 GACTATATAAAGCTGTCAATTTCTGAAGATTTTAAATGGAAAGGGTCATGAACCTTTGAA 300
QY 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
DB 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
QY 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
DB 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
QY 361 AAGGTCAGTTCAATTTGCGGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGCA 420
DB 361 AAGGTCAGTTCAATTTGCGGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGCA 420
QY 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTGTATCTCTCGATGAGCGGTGTGAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTGTATCTCTCGATGAGCGGTGTGAAGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAGACGCTGTCTTAATCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAAGGCTCTGAAGCTGAAGACGCTGTCTTAATCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAAGCCCTGTGACCTACAGGGTACTATGTTGACTCCAAACTGGAT 600
```

```
|||||
DB 541 TACATGGCAAGAAAGCCCTGTGACCTACAGGGTACTATGTTGACTCCAAACTGGAT 600
QY 601 ATAACAAGCACACGAAGACTATACATGCTTGAGAGCATATGAAGAACCGAGGAGCGC 660
DB 601 ATAACAAGCACACGAAGACTATACATGCTTGAGAGCATATGAAGAACCGAGGAGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678
```

```
RESULT 6
US-10-334-288-6
; Sequence 6, Application US/10334288
; Publication No. US20040002123A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: GONZALEZ, Jesus
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
; FILE REFERENCE: REGEN1290-5
; CURRENT APPLICATION NUMBER: US/10/334,288
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/967,772
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 08/765,860
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/ US96/09652
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/481,977
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp "red"
US-10-334-288-6
```

```
Query Match      100.0%; Score 678; DB 16; Length 678;
Best Local Similarity 100.0%; Pred. No. 1,2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTTCATGAGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACGGTCATGCGGACAGAGTTTGAATAGAGCGAAGGAGAGGAGGCGCATACGAAGGC 120
DB 61 ACGGTCATGCGGACAGAGTTTGAATAGAGCGAAGGAGAGGAGGCGCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
QY 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
DB 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGCGGACCTTTGCCATTTTCTTGGGATTT 180
QY 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
DB 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
QY 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
DB 181 TTGTACCAACAATTTCAATATGAGCAAGATATATGTCAAGCAACCTTCCGACATACCA 240
QY 241 GACTATATAAAGCTGTCAATTTCTGAAGATTTTAAATGGAAAGGGTCATGAACCTTTGAA 300
DB 241 GACTATATAAAGCTGTCAATTTCTGAAGATTTTAAATGGAAAGGGTCATGAACCTTTGAA 300
QY 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
DB 301 GACGCTGCGTCTGTACTGTAAACCGAGATTTCAAGTTTGCAGATGCGCTGTTTCATCTAC 360
QY 361 AAGGTCAGTTCAATTTGCGGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
DB 361 AAGGTCAGTTCAATTTGCGGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
```

```

QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTGAATGCGTGTGGAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTGAATGCGTGTGGAAGAGAG 480
QY 481 ATTCTAAGGCTCTGGAAGCTGGAAGAGCGGTGTATCACTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCTAAGGCTCTGGAAGCTGGAAGAGCGGTGTATCACTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGSCAAGAAGCGCTGTGACACTACAGGGTACTACTATGTGTGACTCCAACTGGAT 600
DB 541 TACATGSCAAGAAGCGCTGTGACACTACAGGGTACTACTATGTGTGACTCCAACTGGAT 600
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGAGATGAAAGAACCGAGGAGCGC 660
DB 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGAGATGAAAGAACCGAGGAGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

```

RESULT 7

```

US-09-999-745-66
; Sequence 66, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
US-09-999-745-66

```

Query Match 100.0%; Score 678; DB 9; Length 859;
 Best Local Similarity 100.0%; Pred. No. 1.4e-218;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 60
DB 54 ATGAGGCTTCCAGAAATGTTATCAAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 113
QY 61 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 120
DB 114 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGCTTGGATATT 180
DB 174 CACAATACCGTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGCTTGGATATT 233
QY 181 TTGTACCAACAATTTCAATGATGAAAGCAAGGTATATGCAAGCACTTGCCGACATACCA 240
DB 234 TTGTACCAACAATTTCAATGATGAAAGCAAGGTATATGCAAGCACTTGCCGACATACCA 293
QY 241 GACTATATAAAGCTGTCAATTTCTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA 300
DB 294 GACTATATAAAGCTGTCAATTTCTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA 353
QY 301 GACGCTGCGCTGTACTGTATACCAAGATTCCGTTTGCAAGATGGCTGTTTCACTTAC 360
DB 301 GACGCTGCGCTGTACTGTATACCAAGATTCCGTTTGCAAGATGGCTGTTTCACTTAC 360

```

```

DB 354 GACGCTGCGCTGTACTGTATACCAAGATTCCGTTTGCAAGATGGCTGTTTCACTTAC 413
QY 361 AAGTCAAGTTCAATTTGGCGGTGAACTTTCTTCGATGACCTGTATATGCAAAAGAGACA 420
DB 414 AAGTCAAGTTCAATTTGGCGGTGAACTTTCTTCGATGACCTGTATATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTGAATGCGTGTGGAAGAGAG 480
DB 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTGAATGCGTGTGGAAGAGAG 533
QY 481 ATTCTAAGGCTCTGGAAGCTGGAAGAGCGGTGTATCACTAGTTGAATTCAAAAGTATT 540
DB 534 ATTCTAAGGCTCTGGAAGCTGGAAGAGCGGTGTATCACTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGSCAAGAAGCGCTGTGACACTACAGGGTACTACTATGTGTGACTCCAACTGGAT 600
DB 594 TACATGSCAAGAAGCGCTGTGACACTACAGGGTACTACTATGTGTGACTCCAACTGGAT 653
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGAGATGAAAGAACCGAGGAGCGC 660
DB 654 ATAAACAAGCCACAAGAGACTATACATCGTTGAGAGATGAAAGAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731

```

RESULT 8

```

US-09-866-538-11
; Sequence 11, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEH, Roger
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
US-09-866-538-11

```

Query Match 100.0%; Score 678; DB 10; Length 859;
 Best Local Similarity 100.0%; Pred. No. 1.4e-218;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 60
DB 54 ATGAGGCTTCCAGAAATGTTATCAAGAGTTTCATGAGTTTAAAGTTTCGATGAAAGA 113
QY 61 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 120
DB 114 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGCTTGGATATT 180
DB 174 CACAATACCGTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGCTTGGATATT 233
QY 181 TTGTACCAACAATTTCAATGATGAAAGCAAGGTATATGCAAGCACTTGCCGACATACCA 240
DB 234 TTGTACCAACAATTTCAATGATGAAAGCAAGGTATATGCAAGCACTTGCCGACATACCA 293
QY 241 GACTATATAAAGCTGTCAATTTCTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA 300
DB 294 GACTATATAAAGCTGTCAATTTCTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA 353

```

QY 301 GACGGTGGCTGCTTACTGTAAACCGAGATTCCAGTTTGCAAGATGCGTGTTCATCTAC 360
DB 354 GACGGTGGCTGCTTACTGTAAACCGAGATTCCAGTTTGCAAGATGCGTGTTCATCTAC 413
QY 361 AAGGTCAGTTTCATTTGGGGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGCA 420
DB 414 AAGGTCAGTTTCATTTGGGGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGCA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGGCGTTGAAAGAGAG 480
DB 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGGCGTTTGAAGAGAG 533
QY 481 ATTCATTAAGCTCTGAGCTGAAAGACGCTGCTATTAACCTAGTTGAATCAAAAGATT 540
DB 534 ATTCATTAAGCTCTGAGCTGAAAGACGCTGCTATTAACCTAGTTGAATCAAAAGATT 593
QY 541 TACATGGCAAAAGAGCCGTGTCAGCTACAGGGTATCTATGTTGATCCAACTGGAT 600
DB 594 TACATGGCAAAAGAGCCGTGTCAGCTACAGGGTATCTATGTTGATCCAACTGGAT 653
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAAGAACGAGGACGC 660
DB 654 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAAGAACGAGGACGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731

RESULT 9
US-09-794-308-11
; Sequence 11, Application US/09794308
; Publication No. US20030170911A1

; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: ZACHARIAS, David
; APPLICANT: BAIRD, Geoffrey
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530
; CURRENT APPLICATION NUMBER: US/09-794,308
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: *Discoosoma* sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54) .. (731)
US-09-794-308-11

Query Match 100.0%; Score 678; DB 10; Length 859;
Best Local Similarity 100.0%; Pred. No. 1,4e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTTCTCAAGATGTTATCAAGAGATTCAAGAGTTTAAGTTTCGATGGAAGA 60
DB 54 ATGAGGTTCTCAAGATGTTATCAAGAGATTCAAGAGTTTAAGTTTCGATGGAAGA 113
QY 61 ACGGTCATGGGCAAGAGTTTGAATAGAGCGAAGAGAGGGGAGGCCATACGAAGGC 120
DB 114 ACGGTCATGGGCAAGAGTTTGAATAGAGCGAAGAGAGGGGAGGCCATACGAAGGC 173
QY 121 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATT 180
DB 174 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATT 233
QY 181 TTGTACCAACAATTTAGTATGAGCAAGCAAGGATATATGCAAGCAACCCGCGCAATACCA 240
DB 234 TTGTACCAACAATTTAGTATGAGCAAGCAAGGATATATGCAAGCAACCCGCGCAATACCA 293

QY 241 GACTATAAAAAGCTGTCATTTCTTGAAGATTTAAATGGGAAAGGTCATGAACTTTGAA 300
DB 294 GACTATAAAAAGCTGTCATTTCTTGAAGATTTAAATGGGAAAGGTCATGAACTTTGAA 353
QY 301 GACGGTGGCTGCTTACTGTAAACCGAGATTCCAGTTTGCAAGATGCGTGTTCATCTAC 360
DB 354 GACGGTGGCTGCTTACTGTAAACCGAGATTCCAGTTTGCAAGATGCGTGTTCATCTAC 413
QY 361 AAGGTCAGTTTCATTTGGGGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGCA 420
DB 414 AAGGTCAGTTTCATTTGGGGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGCA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGGCGTTGAAAGAGAG 480
DB 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCTGTATGGCGTTGAAAGAGAG 533
QY 481 ATTCATTAAGCTCTGAGCTGAAAGACGCTGCTATTAACCTAGTTGAATCAAAAGATT 540
DB 534 ATTCATTAAGCTCTGAGCTGAAAGACGCTGCTATTAACCTAGTTGAATCAAAAGATT 593
QY 541 TACATGGCAAAAGAGCCGTGTCAGCTACAGGGTATCTATGTTGATCCAACTGGAT 600
DB 594 TACATGGCAAAAGAGCCGTGTCAGCTACAGGGTATCTATGTTGATCCAACTGGAT 653
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAAGAACGAGGACGC 660
DB 654 ATAAACAAGCCACAAGAGACTATACATCGTTGAGCAGTATGAAAGAACGAGGACGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731

RESULT 10
US-09-865-291-11
; Sequence 11, Application US/09865291
; Publication No. US20030186229A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: TING, Alice
; APPLICANT: ZHANG, Jin
; TITLE OF INVENTION: EMISSION RATIO-METRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: REGEN1550
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: *Discoosoma* sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54) .. (731)
US-09-865-291-11

Query Match 100.0%; Score 678; DB 10; Length 859;
Best Local Similarity 100.0%; Pred. No. 1,4e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTTCTCAAGATGTTATCAAGAGATTCAAGAGTTTAAGTTTCGATGGAAGA 60
DB 54 ATGAGGTTCTCAAGATGTTATCAAGAGATTCAAGAGTTTAAGTTTCGATGGAAGA 113
QY 61 ACGGTCATGGGCAAGAGTTTGAATAGAGCGAAGAGAGGGGAGGCCATACGAAGGC 120
DB 114 ACGGTCATGGGCAAGAGTTTGAATAGAGCGAAGAGAGGGGAGGCCATACGAAGGC 173
QY 121 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATT 180
DB 174 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATT 233


```

QY 181 TTGTACCAATTTTCAGTATGGAAGCAAGTATATGTCAAGCACTTCCGACATACCA 240
DB 234 TTGTACCAATTTTCAGTATGGAAGCAAGTATATGTCAAGCACTTCCGACATACCA 293
QY 241 GACTATTAAGGCTGATTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 300
DB 294 GACTATTAAGGCTGATTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 353
QY 301 GAGCGTGGCTGCTTACTGTATACCAAGATTCAGTTTGAAGATGGCTGTTTCACTAC 360
DB 354 GAGCGTGGCTGCTTACTGTATACCAAGATTCAGTTTGAAGATGGCTGTTTCACTAC 413
QY 361 AAGGTCAAGTTTCATTTGCGTGAACCTTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 420
DB 414 AAGGTCAAGTTTCATTTGCGTGAACCTTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 473
QY 421 AAGCGTGGGAGACCACTGAGCGCTTTGTATCTCTGTATGAGCGCTGTTGAAGAGAG 480
DB 474 AAGCGTGGGAGACCACTGAGCGCTTTGTATCTCTGTATGAGCGCTGTTGAAGAGAG 533
QY 481 ATTCAATAGGCTCTGAGCTGAAGTGAAGACGCTGCTATTAATCAATCAAAAGTATT 540
DB 534 ATTCAATAGGCTCTGAGCTGAAGTGAAGACGCTGCTATTAATCAATCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCCTGTGACGCTTACCAAGGTAATCTATGTTGAATTCGCAAACTGGAT 600
DB 594 TACATGGCAAGAAGCCTGTGACGCTTACCAAGGTAATCTATGTTGAATTCGCAAACTGGAT 653
QY 601 ATAAACAAGCCACAAGCAAGATATACATGTTGAAGAGATTAAGAAACCGAGGAGCGC 660
DB 654 ATAAACAAGCCACAAGCAAGATATACATGTTGAAGAGATTAAGAAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTTAA 678
DB 714 CACCATCTGTTCTTTTAA 731

```

```

RESULT 11
US-10-433-640-12
; Sequence 12, Application US/10433640
; Publication No. US20040115792A1
; GENERAL INFORMATION:
; APPLICANT: Lichtenberg-Frate, Helia
; TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
; FILE REFERENCE: 1487/3
; CURRENT APPLICATION NUMBER: US/10/433, 640
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/14610
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: DE 10061872.3
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discoosoma sp.
; NAME/KEY: CDS
; LOCATION: (54) .. (731)
US-10-433-640-12

```

```

Query Match 100.0%; Score 678; DB 17; Length 859;
Best Local Similarity 100.0%; Pred. No. 1.4e-218; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 54 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTCCGATGGAAGA 113
QY 61 ACGGTCAATGGGCAAGATTGAAATTAAGAGCGAAGAGAGAGGAGCCATACGAAGGC 120

```

```

DB 114 ACGGTCAATGGGCAAGATTGAAATTAAGAGCGAAGAGAGAGGAGCCATACGAAGGC 173
QY 121 CACAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCAATTTGCTGGATATT 180
DB 174 CACAATACCGTAAAGCTTAAAGTAAACCAAGGGGGGACCTTTGCAATTTGCTGGATATT 223
QY 181 TTGTACCAATTTTCAGTATGGAAGCAAGTATATGTCAAGCACTTCCGACATACCA 240
DB 234 TTGTACCAATTTTCAGTATGGAAGCAAGTATATGTCAAGCACTTCCGACATACCA 293
QY 241 GACTATTAAGGCTGATTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 300
DB 294 GACTATTAAGGCTGATTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 353
QY 301 GAGCGTGGCTGCTTACTGTATACCAAGATTCAGTTTGAAGATGGCTGTTTCACTAC 360
DB 354 GAGCGTGGCTGCTTACTGTATACCAAGATTCAGTTTGAAGATGGCTGTTTCACTAC 413
QY 361 AAGGTCAAGTTTCATTTGCGTGAACCTTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 420
DB 414 AAGGTCAAGTTTCATTTGCGTGAACCTTTCCGAGAGATTTAAATGGGAAAGGGTCATGAACCTTGAA 473
QY 421 AAGCGTGGGAGACCACTGAGCGCTTTGTATCTCTGTATGAGCGCTGTTGAAGAGAG 480
DB 474 AAGCGTGGGAGACCACTGAGCGCTTTGTATCTCTGTATGAGCGCTGTTGAAGAGAG 533
QY 481 ATTCAATAGGCTCTGAGCTGAAGTGAAGACGCTGCTATTAATCAATCAAAAGTATT 540
DB 534 ATTCAATAGGCTCTGAGCTGAAGTGAAGACGCTGCTATTAATCAATCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCCTGTGACGCTTACCAAGGTAATCTATGTTGAATTCGCAAACTGGAT 600
DB 594 TACATGGCAAGAAGCCTGTGACGCTTACCAAGGTAATCTATGTTGAATTCGCAAACTGGAT 653
QY 601 ATAAACAAGCCACAAGCAAGATATACATGTTGAAGAGATTAAGAAACCGAGGAGCGC 660
DB 654 ATAAACAAGCCACAAGCAAGATATACATGTTGAAGAGATTAAGAAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTTAA 678
DB 714 CACCATCTGTTCTTTTAA 731

```

```

RESULT 12
US-09-797-496B-3
; Sequence 3, Application US/09797496B
; Publication No. US20030049597A1
; GENERAL INFORMATION:
; APPLICANT: Simon, Sanford M.
; TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
; FILE REFERENCE: 600-1-267
; CURRENT APPLICATION NUMBER: US/09/797, 496B
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3311
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Discoosoma red fluorescent protein modified as described in specif
; OTHER INFORMATION: ication.
US-09-797-496B-3

```

```

Query Match 99.9%; Score 677; DB 10; Length 3311;
Best Local Similarity 100.0%; Pred. No. 6.9e-218; Indels 0; Gaps 0;
Matches 677; Conservative 0; Mismatches 0;
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 289 ATGAGGCTTCCAAAGATGTTATCAAGAGATTCATGAGTTTAAAGTTCCGATGGAAGA 348

```

QY	61	ACGGTCATAGGGCACACAGTTTGAATAATGAAAGCGGAAAGAGAGGGAGGCCATATCGAAGGC	120
Db	349	ACGGTCATAGGGCACACAGTTTGAATAATGAAAGCGGAAAGAGAGGGAGGCCATATCGAAGGC	408
QY	121	CACCAATACCGTAAAGCTTAAGGTATACCAAGGGGGGACCTTTGGCATTTGGCTTGGATATT	180
Db	409	CACCAATACCGTAAAGCTTAAGGTATACCAAGGGGGGACCTTTGGCATTTGGCTTGGGAAATT	468
QY	181	TTGTCAACCAATTTAGTATGAGAGCAGATATATGTCAAGCACCTTGGCCGACATACCA	240
Db	469	TTGTCAACCAATTTAGTATGAGAGCAGATATATGTCAAGCACCTTGGCCGACATACCA	528
QY	241	GACTATAAAAGGTGCATTTCTCGTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA	300
Db	529	GACTATAAAAGGTGCATTTCTCGTGAAGATTAAATGGGAAAGGGTCATGAACCTTTGAA	588
QY	301	GACGGTGGCGCTGTTACTGTAAACCCAGAGATTCCAGTTTGCAGAGATGGCTGTTTCACTAC	360
Db	589	GACGGTGGCGCTGTTACTGTAAACCCAGAGATTCCAGTTTGCAGAGATGGCTGTTTCACTAC	648
QY	361	AAGGTCAAGTTCAATTGGCGTGAACTTTCTTCCGATGGAACCTGTATATGCAAAAGGAACA	420
Db	649	AAGGTCAAGTTCAATTGGCGTGAACTTTCTTCCGATGGAACCTGTATATGCAAAAGGAACA	708
QY	421	ATGGGCTGGGAAAGCCAGACCTGAGCGTTTGATCCTCGTATGGCGGTGGAAGAGAG	480
Db	709	ATGGGCTGGGAAAGCCAGACCTGAGCGTTTGATCCTCGTATGGCGGTGGAAGAGAG	768
QY	481	ATTCTAATAGGCTCTGAAGCTGAAAGACGGTGTGATTAACCTAGTTGAATTCAAAAGTATT	540
Db	769	ATTCTAATAGGCTCTGAAGCTGAAAGACGGTGTGATTAACCTAGTTGAATTCAAAAGTATT	828
QY	541	TACATGGCAAGAGCCTGTGCGACTACCAAGGTACTACTATGTGACCTCCTCAACCTGGAT	600
Db	829	TACATGGCAAGAGCCTGTGCGACTACCAAGGTACTACTATGTGACCTCCTCAACCTGGAT	888
QY	601	ATTAACAAGCCACACGAAAGCTATACATCTGTGAGCAGATGAAAGAACCGAGGAGCGC	660
Db	889	ATTAACAAGCCACACGAAAGCTATACATCTGTGAGCAGATGAAAGAACCGAGGAGCGC	948
QY	661	CACCATCTGTCTCTTTA	677
Db	949	CACCATCTGTCTCTTTA	965

```

RESULT 13
US-10-332-733-22
; Sequence 22, Application US/10332733
; Publication No. US20040106565A1
; GENERAL INFORMATION:
; APPLICANT: Margarette Odenthal and Diana Jung
; TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
; TITLE OF INVENTION: In Myofibroblasts And Myofibroblast-like Cells
; FILE REFERENCE: 1472/66806
; CURRENT APPLICATION NUMBER: US/10/332, 733
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Red
US-10-332-733-22

```

Query Match	98.1%	Score 665	DB 17	Length 666
Best Local Similarity	100.0%	Pred. No. 3.1e-214		
Matches 665; Conservative	0	Mismatches 0	Indels 0	Gaps 0

Db	1	AGAAATGTTTATCAGAGATTCTAGAGTTTAAAGTTTCGATGGAAAGAAACGGTCATAGGG	60
Qy	73	CACGAGTTTGAATATGAAAGGCGAAAGAGAGGGAGGCGCATACGAAGGCCACATATCCGTA	132
Db	61	CACGAGTTTGAATATGAAAGGCGAAAGAGAGGGAGGCGCATACGAAGGCCACATATCCGTA	120
Qy	133	AAAGTTAAAGTAAACCAAGGGGGAGACCTTTCGCAATTTGCTTGGGATATTTTGTGACACAA	192
Db	121	AAAGTTAAAGTAAACCAAGGGGGAGACCTTTCGCAATTTGCTTGGGATATTTTGTGACACAA	180
Qy	193	TTTCAGTATGGAAGCAAGGTATATGTCAAGCAACCCGCGGACATACAGACTATTAAGAAAG	252
Db	181	TTTCAGTATGGAAGCAAGGTATATGTCAAGCAACCCGCGGACATACAGACTATTAAGAAAG	240
Qy	253	CTGTCAATTTCTGAAAGGATTTTAAATGGGAAAGGGTCATGAACCTTTGAAAGCGGTGGCTC	312
Db	241	CTGTCAATTTCTGAAAGGATTTTAAATGGGAAAGGGTCATGAACCTTTGAAAGCGGTGGCTC	300
Qy	313	GTTAAGCTGAACCAAGGATTCAGTTTGCAAGATGGCTGTTTCATCTACAAAGTTCAGTTTC	372
Db	301	GTTAAGCTGAACCAAGGATTCAGTTTGCAAGATGGCTGTTTCATCTACAAAGTTCAGTTTC	360
Qy	373	ATTGGCGTGAACCTTTCCTTCGATGGACCTGTTATGCAAAAGAACATAGGGCTGGGAA	432
Db	361	ATTGGCGTGAACCTTTCCTTCGATGGACCTGTTATGCAAAAGAACATAGGGCTGGGAA	420
Qy	433	GCACAGCACTGAGCGTTTGTATCCTCGTGAATGGCGTGTGAAAGGAGAGATTCATAAGGCT	492
Db	421	GCACAGCACTGAGCGTTTGTATCCTCGTGAATGGCGTGTGAAAGGAGAGATTCATAAGGCT	480
Qy	493	CTGAAGCTGAAGAAGCGGTGCTCATTAAGTGAATTCATAAGTATTTTACATGGCAAG	552
Db	481	CTGAAGCTGAAGAAGCGGTGCTCATTAAGTGAATTCATAAGTATTTTACATGGCAAG	540
Qy	553	AAGCCGTGACACTACAGAGGTACTATGTTGAATCCAAACTGGAATTAACAAGCAC	612
Db	541	AAGCCGTGACACTACAGAGGTACTATGTTGAATCCAAACTGGAATTAACAAGCAC	600
Qy	613	AACGAAGACTATACATCGTTAGCAAGTATGAAGAAGACGAAGGAGCGCACCATCTGTTTC	672
Db	601	AACGAAGACTATACATCGTTAGCAAGTATGAAGAAGACGAAGGAGCGCACCATCTGTTTC	660
Qy	673	CTTTA 677	
Db	661	CTTTA 665	

```

RESULT 14
US-10-314-936-1
/ Sequence 1, Application US/10314936
/ Publication No. US20040110225A1
/ GENERAL INFORMATION:
/ APPLICANT: Gibbs, Patrick D.L.
/ APPLICANT: Carter, Robert W.
/ APPLICANT: Schmale, Michael C.
/ TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
/ FILE REFERENCE: 638.004
/ CURRENT APPLICATION NUMBER: US/10/314,936
/ CURRENT FILING DATE: 2002-12-09
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 711
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: mutant red fluorescent protein
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(711)
/ OTHER INFORMATION:
/ US-10-314-936-1

```

Query Match 97.5%; Score 661; DB 17; Length 711;
 Best Local Similarity 98.5%; Pred. No. 7.2e-213;
 Matches 667; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGCTTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGTTGTTCCAAAGATGTTATCAAGAGCTTCATGAGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACCGTCATGGGACGAGATTGAAATAGAAAGCGAAGAGGAGGAGGACCATACGAAGGC 120
DB 61 ACCGTCATGGGACGAGATTGAAATAGAAAGCGAAGAGGAGGAGGACCATACGAAGGC 120
QY 121 CACAAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180
DB 121 CACAAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180
QY 181 TTGTCAACCAATTTCAAGTATGAGCAAGATATATGTCAAGCACCTTCCGCAATACCA 240
DB 181 TTGTCAACCAATTTCAAGTATGAGCAAGATATATGTCAAGCACCTTCCGCAATACCA 240
QY 241 GACTATATAAAGCTGATTTCTGAAAGATTAAATGGAAGAGGTCATGAACTTTGAA 300
DB 241 GACTATATAAAGCTGATTTCTGAAAGATTAAATGGAAGAGGTCATGAACTTTGAA 300
QY 301 GACGATGCGCTGTTACTGTAAACCAAGATTCCAGTTTGCAGATGCGTGTTCATCTAC 360
DB 301 GACGATGCGCTGTTACTGTAAACCAAGATTCCAGTTTGCAGATGCGTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATTTGCGGAGAACTTTCTTCGATGAGCCTGTATAGCAAAAGACA 420
DB 361 AAGGTCAAGTTCAATTTGCGGAGAACTTTCTTCGATGAGCCTGTATAGCAAAAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTGATGAGCGTGTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTGATGAGCGTGTGAAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTTGCTATTACCTAGTTGAATCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTTGCTATTACCTAGTTGAATCAAAAGTATT 540
QY 541 TACATGCAAAAGAGCTGTGCACTACCAAGGTAATATGTTGACTCCAACTGGAT 600
DB 541 TACATGCAAAAGAGCTGTGCACTACCAAGGTAATATGTTGACTCCAACTGGAT 600
QY 601 ATAAACAAGCCACAAGAACTATACATGTTGAGAGATGATGAAAGAACCGAGGACGC 660
DB 601 ATAAACAAGCCACAAGAACTATACATGTTGAGAGATGATGAAAGAACCGAGGACGC 660
QY 661 CACCATCTGTTCTTTA 677
DB 661 CACCATCTGTTCTTTA 677
    
```

RESULT 15
 US-10-314-936-3
 ; Sequence 3, Application US/10314936
 ; Publication No. US2004011025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gibbs, Patrick D.L.
 ; APPLICANT: Carter, Robert W.
 ; APPLICANT: Schmale, Michael C.
 ; TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
 ; FILE REFERENCE: 638.004
 ; CURRENT APPLICATION NUMBER: US/10/314,936
 ; CURRENT FILING DATE: 2002-12-09
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 711
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:

OTHER INFORMATION: mutant red fluorescent protein
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(711)
 ; OTHER INFORMATION:
 US-10-314-936-3

Query Match 97.5%; Score 661; DB 17; Length 711;
 Best Local Similarity 98.5%; Pred. No. 7.2e-213;
 Matches 667; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGCTTCATGAGTTTAAAGTTCCGATGGAAGA 60
DB 1 ATGAGTTGTTCCAAAGATGTTATCAAGAGCTTCATGAGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACCGTCATGGGACGAGATTGAAATAGAAAGCGAAGAGGAGGACCATACGAAGGC 120
DB 61 ACCGTCATGGGACGAGATTGAAATAGAAAGCGAAGAGGAGGACCATACGAAGGC 120
QY 121 CACAAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180
DB 121 CACAAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180
QY 181 TTGTCAACCAATTTCAAGTATGAGCAAGATATATGTCAAGCACCTTCCGCAATACCA 240
DB 181 TTGTCAACCAATTTCAAGTATGAGCAAGATATATGTCAAGCACCTTCCGCAATACCA 240
QY 241 GACTATATAAAGCTGATTTCTGAAAGATTAAATGGAAGAGGTCATGAACTTTGAA 300
DB 241 GACTATATAAAGCTGATTTCTGAAAGATTAAATGGAAGAGGTCATGAACTTTGAA 300
QY 301 GACGATGCGCTGTTACTGTAAACCAAGATTCCAGTTTGCAGATGCGTGTTCATCTAC 360
DB 301 GACGATGCGCTGTTACTGTAAACCAAGATTCCAGTTTGCAGATGCGTGTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATTTGCGGAGAACTTTCTTCGATGAGCCTGTATAGCAAAAGACA 420
DB 361 AAGGTCAAGTTCAATTTGCGGAGAACTTTCTTCGATGAGCCTGTATAGCAAAAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTGATGAGCGTGTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTGATGAGCGTGTGAAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTTGCTATTACCTAGTTGAATCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTTGCTATTACCTAGTTGAATCAAAAGTATT 540
QY 541 TACATGCAAAAGAGCTGTGCACTACCAAGGTAATATGTTGACTCCAACTGGAT 600
DB 541 TACATGCAAAAGAGCTGTGCACTACCAAGGTAATATGTTGACTCCAACTGGAT 600
QY 601 ATAAACAAGCCACAAGAACTATACATGTTGAGAGATGATGAAAGAACCGAGGACGC 660
DB 601 ATAAACAAGCCACAAGAACTATACATGTTGAGAGATGATGAAAGAACCGAGGACGC 660
QY 661 CACCATCTGTTCTTTA 677
DB 661 CACCATCTGTTCTTTA 677
    
```

Search completed: July 11, 2004, 12:17:49
 Job time: 318 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 08:19:25 ; Search time 305 Seconds
(without alignments)
9443.535 Million cell updates/sec

Title: US-10-006-922a-11

Perfect score: 678
Sequence: 1 atgaagctctccaagaatg.....gccaccatctgtcctta 678

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	AAH47654	Aah47654 Discosoma
2	678	100.0	678	AAD13053	Aad13053 Discosoma
3	678	100.0	678	AAD11142	Aad11142 Discosoma
4	678	100.0	678	ABA95921	Aba95921 Yeast opt
5	678	100.0	678	ADCC24127	Adcc24127 Discosoma
6	678	100.0	859	AAL47952	Aal47952 Discosoma
7	678	100.0	859	AAD53432	Aad53432 Discosoma
8	678	100.0	859	AAD61969	Aad61969 Discosoma
9	677	99.9	3311	ACA62995	Aca62995 Plasmid D
10	665	98.1	666	ABL61142	AbL61142 Red fluor
11	658.8	97.2	898	AAD03615	Aad03615 Discosoma
12	657.2	96.9	898	AAA48742	Aaa48742 Discosoma
13	566.4	83.5	876	AAA28958	Aaa28958 Discosoma
14	566.4	83.5	876	AAD03618	Aad03618 Discosoma
15	566.4	83.5	876	ACCA4649	Acca4649 Red fluor
16	450.6	66.5	723	ABZ22476	Abz22476 Mammalian
17	449.8	66.3	681	AAH47656	Aah47656 Anthozoan
18	449.2	66.3	678	AAD46278	Aad46278 Discosoma
19	449.2	66.3	678	AAD28207	Aad28207 Discosoma
20	449.2	66.3	695	AAA48743	Aaa48743 Humanised
21	447.6	66.0	678	ABA95922	Aba95922 Yeast opt
22	447.2	66.0	681	ADC24134	Adc24134 Discosoma
23	447.2	66.0	4692	AAL47954	Aal47954 Modified

24	447.2	66.0	4692	7	ACCA4640	Acca4640 Vector PD
25	447.2	66.0	7910	4	AAD09979	Aad09979 pB1T(dHSP
26	447.2	66.0	9320	6	ABSS5664	Abss5664 Plasmid p
27	446	65.8	678	6	AAD28208	Aad28208 Discosoma
28	445.8	65.8	6893	9	AAD24111	Aad24111 Proviral
29	445.6	65.7	5436	4	AAD10003	Aad10003 Plasmid p
30	441.2	65.1	678	6	ABA95905	Aba95905 Yeast opt
31	441.2	65.1	678	6	ABA95920	Aba95920 Yeast opt
32	439.6	64.8	678	6	AAD28209	Aad28209 Discosoma
33	439.6	64.6	681	6	ABA95906	Aba95906 Yeast opt
34	438.2	64.6	681	6	ABA95907	Aba95907 Yeast opt
35	438	64.6	678	6	AAD46282	Aad46282 Discosoma
36	436.2	64.3	6985	7	ACA55359	Aca55359 Transform
37	435.6	64.2	675	6	AAD46281	Aad46281 Discosoma
38	434.6	64.1	850	4	AAD03614	Aad03614 Discosoma
39	432.2	63.7	678	9	ADCC24128	Adcc24128 Discosoma
40	410.4	60.5	681	9	ADCC24130	Adcc24130 Discosoma
41	409.6	60.4	699	4	AAH47653	Aah47653 D. striat
42	409.6	60.4	699	4	AAD13052	Aad13052 Discosoma
43	409.6	60.4	699	4	AAD11141	Aad11141 Discosoma
44	409.6	60.4	960	3	AAA28862	Aaa28862 D. striat
45	404	59.6	404	8	AAD38081	Aad38081 DNA of a

ALIGNMENTS

RESULT 1
AAH47654 standard; cDNA; 678 BP.
AC AAH47654;
AC 30-NOV-2001 (first entry)
XX Discosoma sp. red drfp583 protein coding sequence.
XX Fluorescent protein; Anthozoan; fluorescence; marker; FRET; drfp583; ss.
XX Discosoma sp.
XX WO200162919-A1.
XX 30-AUG-2001.
XX 13-FEB-2001; 2001MO-US004625.
XX 23-FEB-2000; 2000US-0184732P.
XX (AURO-) AURORA BIOSCIENCES CORP.
XX Nelson D, Zamaira E, Telen R;
XX WPI; 2001-557704/62.
XX Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise functional red fluorescent proteins, and the encoding nucleic acids, with key mutations for improving the proteins function.
XX Disclosure; Page 83; 90pp; English.
XX The invention provides a nucleic acid encoding functional red fluorescent CC protein (II) that differs from the sequence of an Anthozoan red CC fluorescent protein by at least one amino acid substitution, and with different fluorescent properties. The red fluorescent protein of the CC invention can be expressed by standard recombinant methodology. (II) are used a fluorescent markers and FRET partners. It is used for identifying protein-protein interactions. (II) is also suitable for multiplexed CC fluorescent analysis and FRET-based applications using existing Aegeore CC fluorescent proteins. (II) has improved brightness, reduced spectral CC cross talk, and is rapidly and efficiently expressed in mammalian cells. The key mutations in the encoding nucleic acids provide improved folding, brightness, and create (II) with sharper, more defined excitation and

CC emission peaks when expressed in mammalian cells. The present sequence
CC represents the coding sequence of a Discosoma sp. drfp583 protein, an
XX anthozoan fluorescent protein

Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 ATGAGCTCTTCGAAGATGTTATCAAGAGGATTCATGAGGTTTAAGTTCCGATGGAAGA 60
    |||
Db 1 ATGAGCTCTTCGAAGATGTTATCAAGAGGATTCATGAGGTTTAAGTTCCGATGGAAGA 60
Oy 61 ACGGTCATGCGGACGAGTGTGAATAGAGCGGAGAGAGGGGAGCCATACGAGGC 120
    |||
Db 61 ACGGTCATGCGGACGAGTGTGAATAGAGCGGAGAGAGGGGAGCCATACGAGGC 120
Oy 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
    |||
Db 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
Oy 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
    |||
Db 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
Oy 181 TTGTCAACCAATTTCAATGAGCAAGGATATGTCAAGACCCCTGCCACATACCA 240
    |||
Db 181 TTGTCAACCAATTTCAATGAGCAAGGATATGTCAAGACCCCTGCCACATACCA 240
Oy 241 GACTATAAAGAGCTGTCAATTTCTGAGAGATTTAAATGGGAAAGGGTCATGAACTTTGAA 300
    |||
Db 241 GACTATAAAGAGCTGTCAATTTCTGAGAGATTTAAATGGGAAAGGGTCATGAACTTTGAA 300
Oy 301 GACGTCGCGTCGTACTGTAAACCCAGATTCGATTTGCAAGAGGCTGTTTCACTTAC 360
    |||
Db 301 GACGTCGCGTCGTACTGTAAACCCAGATTCGATTTGCAAGAGGCTGTTTCACTTAC 360
Oy 361 AAGGTCAGTTCATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
    |||
Db 361 AAGGTCAGTTCATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
Oy 421 ATGGCTGGGAAAGCCAGACGAGGCTTGTATCTCTGTATGAGGCTGTGAAGAGAG 480
    |||
Db 421 ATGGCTGGGAAAGCCAGACGAGGCTTGTATCTCTGTATGAGGCTGTGAAGAGAG 480
Oy 481 ATTGTAAGGCTCTGAAAGCTGAAAGACGGTGTCTTACCTTAAGTTGAATTTAAAAAGT 540
    |||
Db 481 ATTGTAAGGCTCTGAAAGCTGAAAGACGGTGTCTTACCTTAAGTTGAATTTAAAAAGT 540
Oy 541 TACATGCGAAAGAGCTGTGACAGCTACCAAGGATCTATGTTGACTCCAACTGAT 600
    |||
Db 541 TACATGCGAAAGAGCTGTGACAGCTACCAAGGATCTATGTTGACTCCAACTGAT 600
Oy 601 ATTAACAGCCCAACGAAGACTATACATCGTTGAGCAAGTAAAGAACCGAGGGACGC 660
    |||
Db 601 ATTAACAGCCCAACGAAGACTATACATCGTTGAGCAAGTAAAGAACCGAGGGACGC 660
Oy 661 CACCATCTGTTCTTTAA 678
    |||
Db 661 CACCATCTGTTCTTTAA 678
```

RESULT 2

AAD13053
ID AAD13053 standard; cDNA, 678 BP.

AAD13053;

16-OCT-2001 (first entry)

XX Discosoma sp. "red" anthozoa fluorescent protein, drfp583 cDNA.
XX Protein destabilisation; linker moiety; reporter moiety; disease model;
XX linear multimerised domain; -NH-ubiquitin protein endoprotease;
KW transgenic animal; transgenic plant; disease resistance;
KW anthozoa fluorescent protein; natural fluorescent protein; ss.

```
XX XX Discosoma sp.  
OS OS  
XX XX  
XX XX WO200157242-A2.  
XX XX  
XX XX 09-AUG-2001.  
XX XX  
XX XX 02-FEB-2001; 2001WO-US003791.  
XX XX  
XX XX 04-FEB-2000; 2000US-00498098.  
XX XX  
XX XX (AURO-) AURORA BIOSCIENCES CORP.  
XX XX  
XX XX Stack JH, Whitney M, Cubitt AB, Pollok BA;  
XX XX WPI; 2001-488890/53.  
XX XX  
XX XX Destabilizing proteins in living cells, by coupling a target protein to  
PT PT linear multimerized destabilization domain non-cleavable by -NH-ubiquitin  
PT PT protein endoproteases, comprising two copies of the domain.  
XX XX  
XX XX Disclosure; Page 110; 171pp; English.
```

The present invention relates to a method for destabilizing a target protein in a cell. The method comprises a linker moiety which operatively couples a target protein (a reporter moiety) to a linear multimerised destabilising domain, which is non-cleavable by a -NH-ubiquitin protein endoprotease. The method is useful for detecting an activity such as protease, protein kinase or phosphoprotein phosphatase activity and is also useful for identifying modulators of these activities. The method is also useful for developing novel assays for a wide range of post-translational activities, such as proteolysis, phosphorylation, dephosphorylation, glycosylation, methylation, sulfation, prenylation, disulfide bond formation and ADP-ribosylation within cells. The recombinant DNA molecule of the invention is useful for creating transgenic animals useful as disease models and transgenic plants with improved disease resistance or other favourable traits. The present sequence is Discosoma sp. "red" anthozoa fluorescent protein, drfp483 cDNA which is a natural fluorescent protein used as a reporter moiety in the exemplification of the invention

Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 ATGAGCTCTTCGAAGATGTTATCAAGAGGATTCATGAGGTTTAAGTTCCGATGGAAGA 60
    |||
Db 1 ATGAGCTCTTCGAAGATGTTATCAAGAGGATTCATGAGGTTTAAGTTCCGATGGAAGA 60
Oy 61 ACGGTCATGCGGACGAGTGTGAATAGAGCGGAGAGAGGGGAGCCATACGAGGC 120
    |||
Db 61 ACGGTCATGCGGACGAGTGTGAATAGAGCGGAGAGAGGGGAGCCATACGAGGC 120
Oy 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
    |||
Db 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
Oy 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
    |||
Db 121 CACATATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTTGGTGGATATT 180
Oy 181 TTGTCAACCAATTTCAATGAGCAAGGATATGTCAAGACCCCTGCCACATACCA 240
    |||
Db 181 TTGTCAACCAATTTCAATGAGCAAGGATATGTCAAGACCCCTGCCACATACCA 240
Oy 241 GACTATAAAGAGCTGTCAATTTCTGAGAGATTTAAATGGGAAAGGGTCATGAACTTTGAA 300
    |||
Db 241 GACTATAAAGAGCTGTCAATTTCTGAGAGATTTAAATGGGAAAGGGTCATGAACTTTGAA 300
Oy 301 GACGTCGCGTCGTACTGTAAACCCAGATTCGATTTGCAAGAGTGGCTGTTTCACTTAC 360
    |||
Db 301 GACGTCGCGTCGTACTGTAAACCCAGATTCGATTTGCAAGAGTGGCTGTTTCACTTAC 360
Oy 361 AAGGTCAGTTCATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
    |||
Db 361 AAGGTCAGTTCATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAGAGACA 420
```

DB 361 AAGTCAAGTTCATTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTTGATCTCGTGTAGCGCTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTTGATCTCGTGTAGCGCTGTTGAAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAGCTGAAGAGACGCTGCTATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAGCTGAAGAGACGCTGCTATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAAAGACCTGTGACGCTACCGAGGACTATGTTGACTGCCAACTGGAT 600
DB 541 TACATGGCAAAAGACCTGTGACGCTACCGAGGACTATGTTGACTGCCAACTGGAT 600
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTAGAGCATATGAAGAACCGAGGACGC 660
DB 601 ATAAACAAGCCACAAGAGACTATACATCGTTAGAGCATATGAAGAACCGAGGACGC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

RESULT 3

AAd1142 standard; DNA; 678 BP.

AAd1142;

24-SEP-2001 (first entry)

Discozona species Anthozoa fluorescent protein, drfp583 encoding DNA.

Transmembrane potential: biological membrane; fluorescent ion; detection;
KM test chemical screening; Anthozoa fluorescent protein; FP;
KM transgenic organism; drfp583 protein; ds.

Discozona sp.

W0200142211-A2.

14-JUN-2001.

12-DEC-2000; 2000WO-US03739.

13-DEC-1999; 99US-00459956.

(REGC) UNIV CALIFORNIA.

Tsiel RY, Gonzalez JE;

WPI; 2001-457276/49.

Determining electrical potential across a membrane in biological systems,
PT comprises introducing two reagents, exposing the membrane to light and
PT measuring the energy transfer.

PS Disclosure; Page 150; 154pp; English.

CC The patent discloses optical methods and compositions for determining
CC transmembrane potential across biological membranes in living cells. The
CC method of determining the electrical potential across a membrane in a
CC biological system comprises introduction of two reagents, a first reagent
CC comprising a hydrophobic fluorescent ion capable of redistributing from a
CC first face of the membrane to a second face of the membrane in response
CC to membrane potential change and a second reagent that label the first
CC face or the second face of the membrane, which comprises a chromophore
CC capable of undergoing energy transfer by either donating or accepting
CC excited state energy to the fluorescent ion. The membrane is then exposed
CC to excitation light and the energy transfer between the reagents is
CC measured and related to the membrane potential. The method is useful for
CC detecting changes in membrane potential in subcellular organelle
CC membranes in biological systems. The method is used for screening of test

CC chemicals for activity to modulate the activity of target ion channel.
CC The invention also provides a transgenic organism comprising a first
CC reagent that comprises a charged hydrophobic fluorescent molecule and a
CC second reagent comprising a bioluminescent or naturally fluorescent
CC protein. The present sequence is Discozona species (red) DNA encoding an
CC Anthozoa fluorescent protein (FP), drfp583

SQ Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 4; Length 678;

Best Local Similarity 100.0%; Pred. No. 7.3e-208; Mismatches 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTCTTCCAAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTGCATGAAAGA 60
DB 1 ATGAGGCTCTTCCAAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTGCATGAAAGA 60
QY 61 ACGGTCAATGGGCAAGGTTTGAATTAAGAGGGAAGAGAGGAGGCGCATACGAAGGC 120
DB 61 ACGGTCAATGGGCAAGGTTTGAATTAAGAGGGAAGAGAGGAGGCGCATACGAAGGC 120
QY 121 CACATATCCGTAAAGCTTAAAGTTAAGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 CACATATCCGTAAAGCTTAAAGTTAAGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 TTGTCAACAATTTCAATGATGAGAGCAAGTATATGTCAGAGCCTTGCATATTTGGATATT 240
DB 181 TTGTCAACAATTTCAATGATGAGAGCAAGTATATGTCAGAGCCTTGCATATTTGGATATT 240
QY 241 GACTATTAATAAGCTGATCTTCTGAAAGATTTAAATGGGAAAGGTCATGAACCTTTGAA 300
DB 241 GACTATTAATAAGCTGATCTTCTGAAAGATTTAAATGGGAAAGGTCATGAACCTTTGAA 300
QY 301 GACGGTGGGCGTGTATCTGTAAACCGAGATTCAGTTTGAGAGTGGCTGTTTCATCTAC 360
DB 301 GACGGTGGGCGTGTATCTGTAAACCGAGATTCAGTTTGAGAGTGGCTGTTTCATCTAC 360
QY 361 AAGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAGACA 420
DB 361 AAGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTTGATCTCGTGTAGCGCTGTTGAAAGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGACCTGAGCGTTTGATCTCGTGTAGCGCTGTTGAAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAGCTGAAGAGACGCTGCTATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAGCTGAAGAGACGCTGCTATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAAAGACCTGTGACGCTACCGAGGACTATGTTGACTGCCAACTGGAT 600
DB 541 TACATGGCAAAAGACCTGTGACGCTACCGAGGACTATGTTGACTGCCAACTGGAT 600
QY 601 ATAAACAAGCCACAAGAGACTATACATCGTTAGAGCATATGAAGAACCGAGGACGC 660
DB 601 ATAAACAAGCCACAAGAGACTATACATCGTTAGAGCATATGAAGAACCGAGGACGC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

RESULT 4
ABA95921 standard; DNA; 678 BP.

ABA95921;

29-MAY-2002 (first entry)

Yeast optimised RFP related DNA SEQ ID NO 18.

Yeast; red fluorescent protein; RFP; plant; transgenic; GFP;

KM	Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana;
XV	Escherichia coli; green fluorescent protein; biotechnology; gene; ss.
XX	
OS	Anthozoa.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..678
FT	/tag= "a
FT	/product= "yeast optimised Red Fluorescent Protein"
PN	DE20001395-U1.
PD	15-MAR-2001.
XX	
PE	27-JAN-2000; 2000DE-02001395.
XX	
PR	27-JAN-2000; 2000DE-02001395.
PA	(GPCB-) GPC BIOTECH AG.
XX	
DR	WPI: 2002-228394/29.
DR	P-PDB; ABB08834.
PT	New DNA encoding red fluorescent protein, useful as marker in
PT	biotechnology, has sequence optimized for expression in eukaryotes,
XX	especially yeast or plants.
PS	Disclosure; Page 14, 19pp; German.
XX	
CC	The invention relates to DNA (1) containing either sequence ABA95905 or
CC	sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein
CC	(YRFP). (1) are used to express red fluorescent protein (RFP) in
CC	eukaryotes, especially yeast, especially Saccharomyces cerevisiae and
CC	plants, especially dicotyledonous plants including Nicotiana tabacum or
CC	Arabidopsis thaliana and also in prokaryotes, especially bacteria,
CC	especially Escherichia coli. RFP is useful in the same way as green
CC	fluorescent protein but is more generally applicable in modern
CC	biotechnology. (1) are optimised for expression in yeast and so generate
CC	RFP at higher levels with stronger fluorescence and thus lowers the
CC	detection limit and gives a better signal-to-noise ratio. The present
CC	sequence is that of a polynucleotide encoding the yeast optimised RFP,
CC	useful to the invention
XX	
SQ	Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;
	Query Match 100.0%; Score 678; DB 6; Length 678;
	Best Local Similarity 100.0%; Pred.No. 7.3e-208;
	Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGAGGTCTTCCAGAATGGTAATCAAGGACTCATGAGTTTAAGATTGCATGGAAGA 60
DB	1 ATGAGGTCTTCCAGAATGGTAATCAAGGACTCATGAGTTTAAGATTGCATGGAAGA 60
QY	61 ACGGTCAATGGGCACGAGTTTGAAATAGAAGCGGAAGAGGAGGACATACGAAGC 120
DB	61 ACGGTCAATGGGCACGAGTTTGAAATAGAAGCGGAAGAGGAGGACATACGAAGC 120
QY	121 CACAATACCCTTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGGCTTGGATAT 180
DB	121 CACAATACCCTTAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTTGGCTTGGATAT 180
QY	181 TTGTACCAACAATTTCAAGTAGGAAGCAAGATATATGTCAAGCACCTTCGCGACATPACA 240
DB	181 TTGTACCAACAATTTCAAGTAGGAAGCAAGATATATGTCAAGCACCTTCGCGACATPACA 240
QY	241 GACATAAAAAAGCTGTCAATTTCTGAAAGATTTAAATGGAAAAGGCTCATGAATTTGAA 300
DB	241 GACATAAAAAAGCTGTCAATTTCTGAAAGATTTAAATGGAAAAGGCTCATGAATTTGAA 300
QY	301 GACGGTGGCGGTGTTAAGTAAACCAAGATTTCCAGTTTGCAGAGATGGCGTTCATCTAC 360
DB	301 GACGGTGGCGGTGTTAAGTAAACCAAGATTTCCAGTTTGCAGAGATGGCGTTCATCTAC 360

Oy	36	AAAGTCAAGTTCATTGCGGTGAACCTTTCCTTCGATGGACCTGTATGCAAAAGAGACA	420
Db	361	AAAGTCAAGTTCATTGCGGTGAACCTTTCCTTCGATGGACCTGTATGCAAAAGAGACA	420
Oy	421	ATGGGCTGGGAAGCCGACGACTGAGCGTTGTATCCTCGTATGCGCTGTGAAAGGAGAG	480
Db	421	ATGGGCTGGGAAGCCGACGACTGAGCGTTGTATCCTCGTATGCGCGTGTGAAAGGAGAG	480
Oy	481	ATTCTATTAAGGCTCTGAAGCTGAAAGAAGCGGTGTCTATTACCTAGTTGAATTCAAAAGATT	540
Db	481	ATTCTATTAAGGCTCTGAAGCTGAAAGAAGCGGTGTCTATTACCTAGTTGAATTCAAAAGATT	540
Oy	541	TACATGGAAGAAAGAGCGCTGTGAGGCTACAGGGGTACTATGTTGACTCCAAATCGAT	600
Db	541	TACATGGAAGAAAGAGCGCTGTGAGGCTACAGGGGTACTATGTTGACTCCAAATCGAT	600
Oy	601	ATTAACAGCCACACACGACAGACTATTAACATCGTTGACGATATGAAGAACGAGGAGCGC	660
Db	601	ATTAACAGCCACACGACAGACTATTAACATCGTTGACGATATGAAGAACGAGGAGCGC	660
Oy	661	CACCATCTGTTCTCTTTAA 678	
Db	661	CACCATCTGTTCTCTTTAA 678	
RESULT 5			
ADCC24127	ID	ADC24127 standard; DNA; 678 BP.	
AC	ADC24127;		
XX	18-DEC-2003	(first entry)	
DE	Discosoma wild-type red fluorescent protein DNA #1.		
XX	Discosoma red fluorescent protein; DsRed; AB interface; AC interface;		
KM	fluorescent protein variant; transcription induction detection;		
KM	fluorescence energy resonance transfer; FRET; protein kinase;		
KM	protein phosphatase; ion indicator; ds.		
OS	Discosoma.		
XX	US2003059835-A1.		
PN	27-MAR-2003.		
PD	10-APR-2002; 2002US-00121258.		
XX	26-FEB-2001; 2001US-00794308.		
FR	24-MAY-2001; 2001US-00866538.		
XX	(TSIE//) TSIE R Y.		
PA	(CAMP//) CAMPBELL R E.		
XX	Tsien RY, Campbell RE;		
EI	WPI; 2003-743764/70.		
DR	P-PSDB; ADC24126.		
XX	Novel polynucleotide sequence encoding Discosoma red fluorescent protein		
PT	variant having a reduced propensity to oligomerize, useful for detecting		
PT	transcriptional activity.		
XX	Example 1; SEQ ID NO 2; 67bp; English.		
XX	The invention describes a polynucleotide sequence (I) encoding a		
CC	Discosoma red fluorescent protein (DsRed) variant having a reduced		
CC	propensity to oligomerize, comprising amino acid substitutions at the AB		
CC	and/or AC interfaces of the wild-type DsRed sequence (SI) comprising 225		
CC	amino acids, given in the specification, where the substitutions result		
CC	in reduced propensity of the DsRed variant to form tetramers. (I) is		
CC	useful for detecting transcriptional activity by providing a host cells		
CC	containing a vector which comprises (I) operatively linked to a		

expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide encoding a fusion protein is useful for the analysis of *in vivo* localisation or trafficking of a polypeptide of interest. A polypeptide marker is useful as markers to identify the location and amount of a target protein produced, where the target protein is fused to the marker, as a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcripts, in applications involving fluorescence energy resonance transfer (FRET), which detects events as the function of the movement of fluorescent donors and acceptors towards or away from each other, for making fluorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as Ca^{2+} , Zn^{2+} , for identifying the presence of a molecule in a sample, for identifying a specific interaction of a first and second molecule, for determining whether a sample contains an enzyme or for determining the pH of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes *Drosophila* wild-type red fluorescent protein.

Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match : 100.0%; Score 678; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 7.3e-208;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGAGGCTTCCAAAGAAAGTTATCAAGAGTTCAAGAGTTTAAAGTTTAAAGTTTGGCATGGAAGA	60
Dp	1	ATGAGGCTTCCAAAGAAAGTTATCAAGAGTTCAAGAGTTTAAAGTTTAAAGTTTGGCATGGAAGA	60
Qy	61	AAGGCAATGGGCGAGAGTTTGAAATAGAAAGCGAAGAGAGGGAGGCGCATTCGAAGCG	120
Dp	61	AAGGCAATGGGCGAGAGTTTGAAATAGAAAGCGAAGAGAGGGAGGCGCATTCGAAGCG	120
Qy	121	CACAAATACCGTAAAGCTTAAAGGTAAACCAAGGGGGAGCTTTTGCATTTGGCTTGGATATT	180
Dp	121	CACAAATACCGTAAAGCTTAAAGGTAAACCAAGGGGGAGCTTTTGCATTTGGCTTGGATATT	180
Qy	181	TTGTGACCAACAAATTCAGATATGGAAGCAAGATATATGTAAGGACCCCTGGCGCATATCCA	240
Dp	181	TTGTGACCAACAAATTCAGATATGGAAGCAAGATATATGTAAGGACCCCTGGCGCATATCCA	240
Qy	241	GACTATATAAAAGCTGTCAATTTCTGAGAGATTTAAATGGAAGAGGTCAATGAACITTTGAA	300
Dp	241	GACTATATAAAAGCTGTCAATTTCTGAGAGATTTAAATGGAAGAGGTCAATGAACITTTGAA	300
Qy	301	GACGGTGGCGTCTTACTGTAAACCCAGAGATTCAGTTTGCAAGATGGCGTTCATCTTAC	360
Dp	301	GACGGTGGCGTCTTACTGTAAACCCAGAGATTCAGTTTGCAAGATGGCGTTCATCTTAC	360
Qy	361	AAGGCAAGTTCATATGGCGGTGAACCTTCCCGATGACCTGTATGTGCAAAAAGAGAACA	420
Dp	361	AAGGCAAGTTCATATGGCGGTGAACCTTCCCGATGACCTGTATGTGCAAAAAGAGAACA	420
Qy	421	ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATTCCTCGTATGGCGGTGTTGAAGSAGAG	480
Dp	421	ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATTCCTCGTATGGCGGTGTTGAAGSAGAG	480
Qy	481	ATTCAATAAGGCTCTGAAGCTGAAGAAACGGTGGTCAATTAACCTAGTTGAATTCAAAAGTATT	540
Dp	481	ATTCAATAAGGCTCTGAAGCTGAAGAAACGGTGGTCAATTAACCTAGTTGAATTCAAAAGTATT	540
Qy	541	TACATGGCAAGAAAGCCTGTGACGCTACCAAGGATCTAATATGTTGACTCCAAACTGGAT	600
Dp	541	TACATGGCAAGAAAGCCTGTGACGCTACCAAGGATCTAATATGTTGACTCCAAACTGGAT	600
Qy	601	ATTACAAAGCCCAACGAAGACCTTACATTCGTTGAGCAATATGAAGAAACCGAGGACCG	660
Dp	601	ATTACAAAGCCCAACGAAGACCTTACATTCGTTGAGCAATATGAAGAAACCGAGGACCG	660
Qy	661	CACCATCTGTTCCCTTAA 678	

Db 661 CACCATCTGTTCCCTTAA 678

AAL47952
 ID AAL47952 standard; DNA; 859 BP.

DT 26-SEP-2002 (first entry)

DE Discosoma red fluorescent protein coding sequence

KW Yeast; RAD54; promoter; genotoxicity cassette; cytotoxicity cassette
KW modified yeast strain; environmental pollution; gene; ds.

OS Discosoma sp.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

PN DE10061872-A1

PD 20-JUN-2002.

PF 12-DEC-2000; 2000DE-01061872.

PR 12-DEC-2000; 2000DE-01061872.

PA (LICH/) LICHTENBERG-FRATE H.

PI Lichtenberg-Frate H;

DR WPT; 2002-539633/58.

XX

PT environment, contains integrated cassettes responsive to genotoxic and

XX

XX

CC integrated stably and functionally in its genome, a genotoxicity cas

CC gene, both of which are different in the two cassettes. The modified

CC genotoxic and/or cytotoxic substances in complex environmental

CC radiation and chemical carcinogens. Particular applications are in

CC toxicology screening and for industrial process control. The present

cc present invention

Sequence 859 BP; 263 A; 163 C; 228 G; 205 T; 0 U; 0 Other;

Query Match	100.0%;	Score 678;	DB 6;	Length 859;
-------------	---------	------------	-------	-------------

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ATGAGGCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTAAGGTCGCATGGAAGA 60

Db 54 ATGAGTCTTCCAAGATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGGAAGA 113

61 ACGGTCATGGGCACGAGTTTGAATAGAGGCCGAGGAGGCCA

Db 114 ACGGTCATGGGCACGAGTTGAAATAGAAAGCGGAAGAG

QY 121 CACATAACCGTAAAGCTTAAGGTAACCAAGGGGACCTTTGCCATTGCTTGGATATT 180

1 ATGAGGCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGTTCCGATGGAAGGA 60

Db 54 ATGAGGCTTCCAAGATGTTATCAAGGAGTTCATGAGTTTAAGGTTCCGATGGAAGGA 11

61 ACGGTCAATGGCAGAGTTTGAATAGAACGCCGAGAGGCCATACGAAGC 120

Db 1.14 ACGTCAATGGCAGAGTTGAATAGAGCGGAGGAGGCCATACGAGGC 1.7

QY 121 CACATATCCGTAAGCTTAAGGTACCAAGGGGACCTTTGCCATTGCTTGGATATT 180


```

RESULT 8
AAD61969
ID AAD61969 standard; cDNA; 859 BP.
XX
AC AAD61969;
XX
DT 15-JAN-2004 (first entry)
XX
DE Discosoma sp. red fluorescent protein (RFP) cDNA.
XX
KM Fluorescent protein; resonance energy transfer; pH; detection;
KW red fluorescent protein; RFP; gene; ss.
XX
OS Discosoma sp.
XX
FH Key Location/Qualifiers
FT CDS 54..731
FT /tag= a
FT /product= "Discosoma sp. red fluorescent protein"
XX
PN US2003170911-A1.
XX
PD 11-SEP-2003.
XX
PF 26-FEB-2001; 2001US-00794308.
XX
PR 26-FEB-2001; 2001US-00794308.
XX
PA (TSIE/) TSIE R. Y.
PA (ZACH/) ZACHARIAS D A.
PA (BAIR/) BAIRD G S.
PI Tsien RY, Zacharias DA, Baird GS;
XX
XX WPI; 2003-802418/75.
DR P-PSDB; ABM00918.
XX
XX Fluorescent proteins containing a mutation that reduces or eliminates its
PT ability to oligomerize which gives more reliable fluorescence resonance
PT energy transfer results and are useful to detect molecule interaction,
PT enzymes, or sample pH.
XX
PS Disclosure; Page 29-30; Opp; English.
XX
XX The invention relates to a non-oligomerizing fluorescent protein
XX containing a mutation that reduces or eliminates its ability to
XX oligomerize. The fluorescent protein gives more reliable fluorescence
XX resonance energy transfer results and are useful to detect molecule
XX interaction, enzymes, or sample pH. These are also used to identify
XX agents or conditions that regulate expression of control sequences. The
XX present sequence is Discosoma sp. red fluorescent protein (RFP) cDNA
XX
SQ Sequence 859 BP; 263 A; 163 C; 228 G; 205 T; 0 U; 0 Other;
Query Match 100.0%; Score 678; DB 9; Length 859;
Best Local Similarity 100.0%; Pred. No. 8.2e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAGAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
DB 54 ATGAGGCTTCCAGAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 113
QY 61 ACGGTCAATGGGCGAGGTTTGAATAGAAAGGCGAAGAGAGGAGGCCATACGAAGGC 120
DB 114 ACGGTCAATGGGCGAGGTTTGAATAGAAATGAAAGGCGAAGAGAGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAAGCTTAAAGTAAACCAAGGGGAGCTTTGCCATTTGCTTGGATATT 180
DB 174 CACAATACCGTAAAGCTTAAAGTAAACCAAGGGGAGCTTTGCCATTTGCTTGGATATT 233
QY 181 TTGTCCACCAATTTGATGATGAAAGCAAGTATATGTCAAGCACTCTGCCGATATCCA 240
|||||

```

```

DB 234 TTGTCCACCAATTTGATGATGAAAGCAAGTATATGTCAAGCACTCTGCCGATATCCA 293
QY 241 GACTATAAAAAGCTGTCATTTCTCTGAAGATTTTAAATGGAAAGGTCATGAACCTTTGAA 300
DB 294 GACTATAAAAAGCTGTCATTTCTCTGAAGATTTTAAATGGAAAGGTCATGAACCTTTGAA 353
QY 301 GACGGTGGCGTCTGTACTGTAAACCAAGATTTCAAGTTTGAAGATGGCTTTTCACTAC 360
DB 354 GACGGTGGCGTCTGTACTGTAAACCAAGATTTCAAGTTTGAAGATGGCTTTTCACTAC 413
QY 361 AAGGTCAAGTTCAATGGCGTGAACCTTTCTCGATGAGACCTTTTATGCAAAAGAGACA 420
DB 414 AAGGTCAAGTTCAATGGCGTGAACCTTTCTCGATGAGACCTTTTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGAGCGTGTGAAGAGAG 480
DB 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGAGCGTGTGAAGAGAG 533
QY 481 ATTCATTAAGCTCTGAAGCTGAAAAGCGTGTATTAACCTTAATTGAATTCAAAAGTATT 540
DB 534 ATTCATTAAGCTCTGAAGCTGAAAAGCGTGTATTAACCTTAATTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAAGAGCGTGTGAGCTTACCAAGGTACTATGTTGACTGCAAACTGGAT 600
DB 594 TACATGGCAAAGAGCGTGTGAGCTTACCAAGGTACTATGTTGACTGCAAACTGGAT 653
QY 601 ATTAACAAGCCACAACAGACATAACATGCTTTAGACAGATGAAAACCGAGGAGCGC 660
DB 654 ATTAACAAGCCACAACAGACATAACATGCTTTAGACAGATGAAAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731

RESULT 9
ACA62995
ID ACA62995 standard; DNA; 3311 BP.
XX
XX ACA62995;
AC
XX
DT 23-SEP-2003 (first entry)
XX
XX Plasmid DNA containing coding sequence for RFP.
DE
XX
XX Fluorescently-tagged enzyme; substrate; cell population; GFP;
KW quantification of enzymatic activity; green fluorescent protein;
KW red fluorescent protein; RFP; enhanced green fluorescent protein; EGFP;
KW enzymatic process; cellular enzyme; chemotherapeutic drug;
KW multidrug resistance; MDR; ds.
XX
OS Aequorea victoria.
XX
XX Synthetic.
XX
XX US2003049597-A1.
XX
XX 13-MAR-2003.
XX
XX 01-MAR-2001; 2001US-00797496.
XX
XX 01-MAR-2001; 2001US-00797496.
XX
XX (SIMO/) SIMON S M.
XX (CHEN/) CHEN Y.
XX
XX Simon SM, Chen Y;
XX
XX WPI; 2003-555145/52.
DR
XX
XX Simultaneously quantifying in situ the relationship between an enzyme and
PT its substrate for study of enzymatic processes at a cellular level,
PT comprises optical measurements on cells expressing the fluorescently
PT tagged enzyme.

```

XX Disclosure; Page 8-9; 21pp; English.
XX
XX The present invention relates to a method for simultaneously quantifying
CC in situ the relationship between a fluorescently-tagged enzyme (E) and
CC its substrate in a population of cells. A population of cells expressing
CC (E) is created in which different cells contain different amounts of (E).
CC The cells are incubated with a substrate, and the concentration and
CC enzymatic activity of (E) in each cell are simultaneously quantified by
CC optical means. The fluorescently-tagged enzyme is produced by linking the
CC enzyme with Aequorea victoria green fluorescent protein (GFP), or its
CC variants or derivatives such as red fluorescent protein (RFP) and
CC enhanced green fluorescent protein (EGFP). The method of the invention is
CC useful for simultaneously quantifying in situ the relationship between an
CC enzyme and its substrate in a cell. The method is useful for the study of
CC the interactions of cellular enzymes with chemotherapeutic drugs, e.g.,
CC for elucidating mechanisms of multidrug resistance (MDR). The present
CC sequence represents a plasmid containing the coding sequence for RFP
XX
XX Sequence 3311 BP; 858 A; 778 C; 860 G; 815 T; 0 U; 0 Other;

Query Match 99.9%; Score 677; DB 8; Length 3311;

Best Local Similarity 100.0%; Pred. No. 3,4e-207; Mismatches 0; Gaps 0;
Matches 677; Conservative 0; Indels 0;

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 60
DB 289 ATGAGGCTTCCAGAAATGTTATCAAGAGTTCAAGGTTTAAAGTTCCGATGGAAGA 348
QY 61 ACGGTCATGGGACGAGATTGAAATAGAGCCAGAGAGAGGGAGCCCTACGAAAGGC 120
DB 349 ACGGTCATGGGACGAGATTGAAATAGAGCCAGAGAGAGGGAGCCCTACGAAAGGC 408
QY 121 CACATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTTGGCCATTGCTTGGGATTT 180
DB 409 CACATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTTGGCCATTGCTTGGGATTT 468
QY 181 TTGTACCAACAATTTCAATATGATGAAAGAGTATATGCAAGACCCCTGCGACATACCA 240
DB 469 TTGTACCAACAATTTCAATATGATGAAAGAGTATATGCAAGACCCCTGCGACATACCA 528
QY 241 GACATTAATAAGGCTGCTTTCTCGAAGAGATTAAATGGGAAAGGTTATGAACCTTTGAA 300
DB 529 GACATTAATAAGGCTGCTTTCTCGAAGAGATTAAATGGGAAAGGTTATGAACCTTTGAA 588
QY 301 GACGCTGCGCTGTTACTGTAAACCAAGGATTCAGATTGCAAGATGCTGTTTCTATC 360
DB 589 GACGCTGCGCTGTTACTGTAAACCAAGGATTCAGATTGCAAGATGCTGTTTCTATC 648
QY 361 AAGGTCAAGTTCAATGGGCTGAACCTTTCCGATGACCTGTTATGCAAAAGAGACA 420
DB 649 AAGGTCAAGTTCAATGGGCTGAACCTTTCCGATGACCTGTTATGCAAAAGAGACA 708
QY 421 ATGGGCTGGGAGAGCCAGACCTGAGGTTTGTATCTCTGTATGGCGTGTGAAAGAGAG 480
DB 709 ATGGGCTGGGAGAGCCAGACCTGAGGTTTGTATCTCTGTATGGCGTGTGAAAGAGAG 768
QY 481 ATTCAATAAGGCTGTAAGCTGAAGAAGCGGTGTCATTACTAGTTGAATCAAAAGTAT 540
DB 769 ATTCAATAAGGCTGTAAGCTGAAGAAGCGGTGTCATTACTAGTTGAATCAAAAGTAT 828
QY 541 TACATGGCAAGAAAGCCTGTGACAGTACAGGGTATCTATATGTTGACTCCAAATCGAT 600
DB 829 TACATGGCAAGAAAGCCTGTGACAGTACAGGGTATCTATATGTTGACTCCAAATCGAT 888
QY 601 ATAACAAGCCCAAGAGACTATATCATCTGTGAGCGTATGAAGAAACCGAGGAGAGC 660
DB 889 ATAACAAGCCCAAGAGACTATATCATCTGTGAGCGTATGAAGAAACCGAGGAGAGC 948
QY 661 CACCATCTGTTCTTTA 677
DB 949 CACCATCTGTTCTTTA 965

RESULT 10

ABL61142
ID ABL61142 standard; DNA; 666 BP.

XX
XX ABL61142;

AC 18-SEP-2002 (first entry)

DE Red fluorescent protein reporter DNA fragment.

KM Alpha-SMA; smooth muscle actin; screening; smooth muscle cell;

KM myofibroblast; gene therapy; red fluorescent protein; db.

OS Synthetic.

XX EPI172375-A1.

XX 16-JAN-2002.

XX 22-DEC-2000; 2000EP-00128446.

XX 11-JUL-2000; 2000DE-01033633.

XX 31-OCT-2000; 2000DE-01053879.

XX (ODEN/) ODENTHAL M.

XX Odenthal M, Jung D;

XX WPI; 2002-149590/20.

XX New nucleic acid containing regulatory region of the smooth muscle actin

XX gene, useful e.g. for manipulating gene expression in smooth muscle

XX cells.

XX Disclosure; Page 20; 44pp; German.

XX This invention describes a novel nucleic acid (I) comprising: (i) at

XX least one functional region (Ia) from the regulatory region of the alpha-

XX smooth muscle actin (SMA) gene and (ii) at least one additional

XX functional sequence (Ib) operably linked to (Ia). The products of the

XX invention can be used for preparing genetically modified eukaryotic cells

XX or organisms, for isolation and screening of smooth muscle cells,

XX myofibroblasts or related cells, and for manipulation of gene expression

XX and/or cell function in smooth muscle cell or myofibroblasts,

XX particularly for gene therapy. Component (Ia) provides cell-type- or

XX differentiation-specific expression or modulation of genes. This sequence

XX represents a DNA fragment of red fluorescent protein (EGFP) which can be

XX used as a reporter molecule under the control of the alpha-SMA described

XX in the invention

XX Sequence 666 BP; 202 A; 126 C; 176 G; 162 T; 0 U; 0 Other;

QY Query Match 98.1%; Score 665; DB 6; Length 666;

Best Local Similarity 100.0%; Pred. No. 1.1e-203;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AAGATGTTATCAAGAGGTTCAATGAGTTTAAAGTTTCGATGGAAGAAAGCGTCAATGG 72
DB 1 AAGATGTTATCAAGAGGTTCAATGAGTTTAAAGTTTTCGATGGAAGAAAGCGTCAATGG 60
QY 73 CACGAGTTTAAATAGAAAGCGAAGAGAGGAGGCGCATACGAAGGCCAATACCGTA 132
DB 61 CACGAGTTTAAATAGAAAGCGAAGAGAGGAGGCGCATACGAAGGCCAATACCGTA 120
QY 133 AAGCTTAAGGTAAACCAAGGGGGGACCTTTGCGCATTTGCTTGGATATTTTGTACACCAA 192
DB 121 AAGCTTAAGGTAAACCAAGGGGGGACCTTTGCGCATTTGCTTGGATATTTTGTACACCAA 180
QY 193 TTTCAAGTAAAGCAAGGATATATGTCAGACACCTGCGGACATACGACTATTAAG 252
DB 181 TTTCAAGTAAAGCAAGGATATATGTCAGACACCTGCGGACATACGACTATTAAG 240

```
QY 253 CTGTCATTTCTGAGAGATTTAAATGAGAAAGGTCATGAACTTTGAAGACGCTGGCGTC 312
Db 241 CTGTCATTTCTGAGAGATTTAAATGAGAAAGGTCATGAACTTTGAAGACGCTGGCGTC 300
QY 313 GTTACCTGAACCCGAGATTCAGTTTTCAGAGATGCGCTTTCATCTCAAGGTCAAGTTC 372
Db 301 GTTACCTGAACCCGAGATTCAGTTTTCAGAGATGCGCTTTCATCTCAAGGTCAAGTTC 360
QY 373 ATTGGCTGAACCTTCTCTCCGATGACCTGTATGCAAAAGACAAATGGCTGGGAA 432
Db 361 ATTGGCTGAACCTTCTCTCCGATGACCTGTATGCAAAAGACAAATGGCTGGGAA 420
QY 433 GCCAGCACTGAGCGCTTTGTATCTCGTGAATGCGCTTTGAAAGAGAGATTCATAGGCT 492
Db 421 GCCAGCACTGAGCGCTTTGTATCTCGTGAATGCGCTTTGAAAGAGAGATTCATAGGCT 480
QY 493 CTGAAGCTGAAAGACGCTGTGCTATTCCTAGTTGAATTCAAATAATTTTACATGGCAAG 552
Db 481 CTGAAGCTGAAAGACGCTGTGCTATTCCTAGTTGAATTCAAATAATTTTACATGGCAAG 540
QY 553 AAGCTGTGACGCTACCGAGGCTACTATGTTGACTGCCAACTGATATATCAAGCCAC 612
Db 541 AAGCTGTGACGCTACCGAGGCTACTATGTTGACTGCCAACTGATATATCAAGCCAC 600
QY 613 AACGAGACTATATACATCTGTTGACAGATGAAAGAACCGAGGACCGCACATCTGTTC 672
Db 601 AACGAGACTATATACATCTGTTGACAGATGAAAGAACCGAGGACCGCACATCTGTTC 660
QY 673 CTTTA 677
Db 661 CTTTA 665
```

RESULT 11

ID AAD03615 standard; cDNA; 898 BP.

XX AAD03615;

DT 11-SEP-2003 (revised)
DT 19-JUN-2001 (first entry)

XX Discosoma sp. red chromo/fluorescent protein, dirFP583 (NFP-6) cDNA.

XX Anthrozoa; Chromoprotein; fluorescent protein; dirFP583; NFP-6; sunscreen;
KM analyte detection assay; selectable marker; recombinant DNA application;
KM biosensor; pH indicator; invivo marker; selective filter; ss.

XX Discosoma sp; red.

XX OS
XX FH Key Location/Qualifiers
XX FT CDS 93..770FT /*tag= a
FT /product= "Chromo/fluorescent protein, dirFP583 (NFP-6)"
FT /transl_except= (pos:540..600, aa:Leu-gly)
FT /note= "Insertion of 60 bases alters the reading frame"

XX MO200127150-A2.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028477.

XX 14-OCT-1999; 99US-00418529.

XX 15-OCT-1999; 99US-00418917.

XX 15-OCT-1999; 99US-00418922.

XX 19-NOV-1999; 99US-0044338.

XX 19-NOV-1999; 99US-0044341.

XX 09-DEC-1999; 99US-00457556.

XX 09-DEC-1999; 99US-00457698.

XX 09-DEC-1999; 99US-00458144.

```
PR 10-DEC-1999; 99MO-US029405.  
PR 14-JUN-2000; 2000US-0211607P.  
PR 14-JUN-2000; 2000US-0211609P.  
PR 14-JUN-2000; 2000US-0211626P.  
PR 14-JUN-2000; 2000US-0211627P.  
PR 14-JUN-2000; 2000US-0211687P.  
PR 14-JUN-2000; 2000US-0211766P.  
PR 14-JUN-2000; 2000US-0211880P.  
PR 14-JUN-2000; 2000US-0211888P.  
PR 14-JUN-2000; 2000US-0212070P.
```

XX (CLON-) CLONTECH LAB INC.

XX Lukyanov SA, Fradkov AE, Labas YA, Matz MV, Tersikh A;

XX WPI; 2001-266409/27.

XX P-PSDB; AAE00375.

XX An Anthrozoa chromo- or fluorescent protein (Pl) present in an environment

XX other than its natural environment, useful as a label in analyte

XX detection assays and as a selectable marker in recombinant DNA

XX applications.

XX Claim 13; Fig 6; 69pp; English.

XX The present sequence is a Discosoma sp. red chromo/fluorescent protein,

XX dirFP583 (NFP-6) cDNA. NFP-6 is present in an environment other than its

XX natural environment and has an absorbance maximum ranging from 250nm to

XX 750nm and more usually from 540nm to 580nm and emission maximum ranging

XX from 275nm to 775nm and more usually from 565 to 605nm. The

XX chromoproteins or fluorescent proteins are useful as labels in analyte

XX detection assays, as selectable markers in recombinant DNA applications,

XX as biosensors in prokaryotic and eukaryotic cells e.g. as pH indicator

XX and as in vivo markers in animals. They are also useful in sunscreens and

XX as selective filters. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 898 BP; 273 A; 173 C; 240 G; 212 T; 0 U; 0 Other;

SQ Query Match 97.2%; Score 658.8; DB 4; Length 898;

Best Local Similarity 98.2%; Pred. No. 1.3e-201;

Matches 666; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAGAGATGTTATCAAGAGTTCATGAGTTTAAAGTTTGCATGGAAGCA 60

Db 93 ATGAGGCTTCCAGAGATGTTATCAAGAGTTCATGAGTTTAAAGTTTGCATGGAAGCA 152

QY 61 ACGTCAATGGGACGAGTTTGAATGAAGGAGGAGGAGGAGGCCATACGAAGGC 120

Db 153 ACGTCAATGGGACGAGTTTGAATGAAGGAGGAGGAGGAGGCCATACGAAGGC 212

QY 121 CACAATACGCTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGATTT 180

Db 213 CACAATACGCTAAAGCTTAAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGATTT 272

QY 181 TTGTCAACCAATTTCAATGTAAGAGCAAGTATATGTCAGACACCTTCCGACATACCA 240

Db 273 TTGTCAACCAATTTCAATGTAAGAGCAAGTATATGTCAGACACCTTCCGACATACCA 332

QY 241 GACTATTAAGAGTTCATTTCTGTAAGAGATTTAAATGGAAGGAGGATGGAAGCTTTGAA 300

Db 333 GACTATTAAGAGTTCATTTCTGTAAGAGATTTAAATGGAAGGAGGATGGAAGCTTTGAA 392

QY 301 GACGTCGCTGCTTACTGTAACCAAGATTCAGTTTGAAGAGGAGGAGGAGGATTTATC 360

Db 393 GACGTCGCTGCTTACTGTAACCAAGATTCAGTTTGAAGAGGAGGAGGAGGATTTATC 452

QY 361 AAGTCAAGTTCAATGCGGTGAACCTTCTCCGATGACCTTTATGCAAAAGAGACA 420

Db 453 AAGTCAAGTTCAATGCGGTGAACCTTCTCCGATGACCTTTATGCAAAAGAGACA 512

QY 421 ATGGGCTGGGAAGCCGACCTGAGCGTTGTATCTCGATGAGGAGGAGGAGGAGGAG 480

Db 513 ATGGGCTGGGAAGCCGACCTGAGCGTTGTATCTCGATGAGGAGGAGGAGGAGGAG 572

```
Qy 481 ATTCATTAAGGCTCTGAGAGCTGAAAGACGCTGGTCACTTAAGTGAATTCAAAAGTATT 540
D 573 ATTGATTAAGGCTCTGAGAGCTGAAAGACGCTGGTCACTTAAGTGAATTCAAAAGTATT 632
Qy 541 TACATGCAAGAAAGCTGTGAGCTACCAAGGATCTACTATGTTGACTCCAAATCGAT 600
D 633 TACATGCAAGAAAGCTGTGAGCTACCAAGGATCTACTATGTTGACTCCAAATCGAT 692
Qy 601 ATTAACAAGCCCAACGAAGACTATACATCGTTGAGAGTATGAAAGAACGAGGAGCGC 660
D 693 ATTAACAAGCCCAACGAAGACTATACATCGTTGAGAGTATGAAAGAACGAGGAGCGC 752
Qy 661 CACCATCTGTTCTTTAA 678
D 753 CACCATCTGTTCTTTAA 770

RESULT 12
AAA48742
ID AAA48742 standard; cDNA; 898 BP.
XX AC
XX AAA48742;
XX
DT 15-SEP-2003 (revised)
DT 19-SEP-2000 (first entry)
DE Discosoma sp. "red" novel fluorescent protein drfp583 cDNA.
XX Anchozoa; drfp583; fluorescent protein; non-bioluminescent organism;
XX fluorescent labeling; ss.
XX Discosoma sp; "red".
XX OS
XX Key Location/Qualifiers
FH 93.770
FT CDS /product= "drfp583"
FT /transl_except= (pos:456..457,aa:Val)
FT /transl_except= (pos:470..473,aa:Val)
FT /note= "The codon at position 456..457 has an apparent 1
FT nucleotide deletion which alters the reading frame. The
FT codon at position 470..473 has an apparent 1 nucleotide
FT insertion which corrects the altered reading frame"
XX
XX MO200034326-A1.
XX
XX 15-JUN-2000.
XX
XX 10-DEC-1999; 99MO-US029473.
XX
XX 11-DEC-1998; 98US-00210330.
XX 14-OCT-1999; 99US-00418529.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Lukyanov SA, Fradkov AF, Labas YA, Matz MV, Green G, Chen Y;
XX Ding L;
XX MPI; 2000-423381/36.
XX
XX Novel fluorescent protein from non-bioluminescent Discosoma sp. red,
XX useful for fluorescent labeling and as markers.
XX
XX Claim 6; Page 73-74; 86pp; English.
XX
XX The present sequence is the cDNA sequence of drfp583 from Discosoma sp.
XX "red", a non-bioluminescent species of the Class Anchozoa. drfp583 is a
XX full-length cDNA encoding a novel fluorescent protein (nfp). Fluorescent
XX proteins can be used in fluorescent labeling, a useful tool for marking a
XX protein, cell or organism of interest. Unlike other markers used in
XX protein labeling, such as beta-galactosidase and luciferase, fluorescent
XX proteins do not require an exogenous cofactor or substrate. Methods
XX involving fluorescent proteins are also less laborious and less difficult
```

```
CC to control than the traditional methods of fluorescent labeling, where a
CC protein of interest is purified and then covalently conjugated to a
CC fluorophore derivative. Novel fluorescent proteins isolated from species
CC of the Class Anchozoa can be used as markers for gene expression and
CC protein localization studies, and in fluorescence resonance energy
CC transfer (FRET) reactions. They may have improved properties and better
CC suitability for larger excitations compared to prior art fluorescent
CC proteins such as green fluorescent protein. (Updated on 15-SEP-2003 to
CC standardise OS field)
XX
XX Sequence 898 BP; 273 A; 172 C; 240 G; 213 T; 0 U; 0 Other;
XX
XX Query Match 96.9%; Score 657.2; DB 3; Length 898;
XX Best Local Similarity 98.1%; Pred. No. 4.3e-201;
XX Matches 665; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1 ATGAGGCTTCCAAAGATGTTATCAAGAGAGTCATGAGTTTAAAGTTCGATGAAAGA 60
D 93 ATGAGGCTTCCAAAGATGTTATCAAGAGAGTCATGAGTTTAAAGTTCGATGAAAGA 152
Qy 61 ACGGTCAATGGGCAAGATTGAAATGAAGCGGAAGAGAGGAGCCATACGAAGGC 120
D 153 ACGGTCAATGGGCAAGATTGAAATGAAGCGGAAGAGAGGAGCCATACGAAGGC 212
Qy 121 CACAAATCCGTAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180
D 213 CACAAATCCGTAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 272
Qy 181 TTGTACACCAAAATTCAGTATGGAAGCAAGTAAATGATCAAGCAACCTCGCATCA 240
D 273 TTGTACACCAAAATTCAGTATGGAAGCAAGTAAATGATCAAGCAACCTCGCATCA 332
Qy 241 GACTATTAAGGCTGTCATTTCTGAAAGATTAAATGGAAGAGGTCATGAACCTTTGAA 300
D 333 GACTATTAAGGCTGTCATTTCTGAAAGATTAAATGGAAGAGGTCATGAACCTTTGAA 392
Qy 301 GACGTCGCGCTGCTGATCTGTAACCCAGAGATTCAGATTGAGAGATGCTGTTCACTAC 360
D 393 GACGTCGCGCTGCTGATCTGTAACCCAGAGATTCAGATTGAGAGATGCTGTTCACTAC 452
Qy 361 AAGGTCAAGTTCAATGCGTGAACCTTCCGATGAGACCTGTATGCAAAAGAGACA 420
D 453 AAGGTCAAGTTCAATGCGTGAACCTTCCGATGAGACCTGTATGCAAAAGAGACA 512
Qy 421 ATGGGCTGGGAAGCCAGACTGAGCGTTGTATCTCTGTATGAGCGTGTGAAAGAGAG 480
D 513 ATGGGCTGGGAAGCCAGACTGAGCGTTGTATCTCTGTATGAGCGTGTGAAAGAGAG 572
Qy 481 ATTGATTAAGGCTCTGAGAGCTGAAAGACGCTGGTCACTTAAGTGAATTCAAAAGTATT 540
D 573 ATTGATTAAGGCTCTGAGAGCTGAAAGACGCTGGTCACTTAAGTGAATTCAAAAGTATT 632
Qy 541 TACATGCAAGAAAGCTGTGAGCTACCAAGGATCTACTATGTTGACTCCAAATCGAT 600
D 633 TACATGCAAGAAAGCTGTGAGCTACCAAGGATCTACTATGTTGACTCCAAATCGAT 692
Qy 601 ATTAACAAGCCCAACGAAGACTATACATCGTTGAGAGTATGAAAGAACGAGGAGCGC 660
D 693 ATTAACAAGCCCAACGAAGACTATACATCGTTGAGAGTATGAAAGAACGAGGAGCGC 752
Qy 661 CACCATCTGTTCTTTAA 678
D 753 CACCATCTGTTCTTTAA 770

RESULT 13
AAA28958
ID AAA28958 standard; cDNA; 876 BP.
XX AC
XX AAA28958;
XX
DT 12-SEP-2000 (first entry)
```

DE Discosoma sp. "magenta" dmfp592 cDNA encoding a fluorescent protein.
 XX dmfp592; fluorescent protein; non-bioluminescent; label; marker;
 KM fluorescence resonance energy transfer reaction; FRRT; ss.
 KW
 OS Discosoma sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..737
 FT /tag= a
 FT /product= "fluorescent_protein"
 PN WO200034324-A1.
 PD 15-JUN-2000.
 XX
 PF 10-DEC-1999; 99MO-US029412.
 XX
 PR 11-DEC-1998; 98US-00210330.
 PR 19-NOV-1999; 99US-00444341.
 XX
 PA (CLON-) CLONTECH LAB INC.
 PI Lukyanov SA, Fradkov AF, Labas YA, Matz MV;
 DR WPI; 2000-423379/36.
 XX P-PSDB; AAY92894.
 PT Novel fluorescent protein from non-bioluminescent Discosoma species,
 PT useful for fluorescent labeling and as markers.
 XX
 PS Claim 7; Page 54-55; 60pp; English.
 XX
 CC This cDNA encodes a fluorescent protein (dmfp592) from Discosoma sp.
 CC "magenta", a non-bioluminescent species of the genera Anthozoa. The
 CC fluorescent colour is observed under usual light or ultraviolet
 CC light. It has an absorbance maximum at 573 nm and an emission maximum at
 CC 593 nm. The polynucleotides of the invention can be used to produce the
 CC proteins recombinantly, and as a source of primers and probes for
 CC identifying related proteins. The fluorescent proteins have applications
 CC in fluorescent labeling, as fluorescent markers for gene expression and
 CC protein localization studies, and in fluorescence resonance energy
 CC transfer (FRRT) reactions. They may have improved properties and better
 CC suitability for larger excitations, compared to prior art fluorescent
 CC proteins such as green fluorescent protein from *Aequorea victoria*, which
 CC has an excitation maximum at 395 nm, a second excitation peak at 475 nm
 CC and an emission maximum at 510 nm.
 CC
 SQ Sequence 876 BP; 256 A; 165 C; 232 G; 223 T; 0 U; 0 Other;
 Query Match 83.5%; Score 566.4; DB 3; Length 876;
 Best Local Similarity 90.6%; Pred. No. 8.3e-172;
 Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
 QY 1 ATGAGTCTTCCAGAAATGTTATCAAGAGATTCAAGGTTTAAAGTTTCGATGAAAGA 60
 DB 45 ATGAGTCTTCCAGAAATGTTATCAAGAGATTCAAGGTTTAAAGTTTCGATGAAAGA 104
 QY 61 ACGGTAATGGGCGAGGTTGAATTAAGAGCGAAGAGAGGGGAGCCATACGAAGGC 120
 DB 105 ACGGTAATGGGCGAGGTTGAATTAAGAGCGAAGAGAGGGGAGCCATACGAAGGC 164
 QY 121 CACAATACCGTAAGGTTAAGGTAACCAAGGGGGGAGCCTTGGCATTGGCTGGGATATT 180
 DB 165 CACTGTTCCGTAAGGTTAAGGTAACCAAGGGGGGAGCCTTGGCATTGGCTGGGATATT 224
 QY 181 TTGTACCAACAATTTAGATGAGCAAGGATATATGTCAGACCCCTGCCGACATACCA 240
 DB 225 TTGTACCAACAATTTAGATGAGCAAGGATATATGTCAGACCCCTGCCGACATACCA 284
 QY 241 GACTATATAAAGGCTGCTATTTCTGGAAGATTTAAATGGGAAAGGCTCATGAACCTTTGAA 300
 DB 285 GACTATATAAAGGCTGCTATTTCTGGAAGATTTAAATGGGAAAGGCTCATGAACCTTTGAA 344

QY 301 GACGGTGGCGTCTGTTACTGTAACCCAGATTCCAGATTGCGAGATGCTGTTTCATCTAC 360
 DB 345 GACGGTGGCGTCTGTTACTGTAACCCAGATTCCAGATTGCGAGATGCGAGATGCTGTTTCATCTAC 404
 QY 361 AAGTCAAGTTTCAATGAGCTGTAACCTTCTCCGATGAGCCTGTTATGCAAGAAAGAGACA 420
 DB 405 AAGTCAAGTTTCAATGAGCTGTAACCTTCTCCGATGAGCCTGTTATGCAAGAAAGAGACA 464
 QY 421 ATGGGCTGGGAAGCCGACGACTGAGCGTTGTAACCTGATGAGCGTGTGGAAGAGAG 480
 DB 465 CGGGGCTGGGAAGCCGACGCTGAGCGTTGTAACCTGATGAGCGTGTGGAAGAGAG 524
 QY 481 ATTCAATAGGCTCTGAAAGCTGAAAGACGGTGTCAATTAACCTTAAGTTCAAAAGTATT 540
 DB 525 ATCAATATGAGCTCTGAGCTGGAAGAGCGGACATTAACCTGTAATTAACAAAGTATT 584
 QY 541 TACATGGCAAAAGAGCT--GTGAGCTAACCAAGGTAATTAATTTGATCCCAACG 597
 DB 585 TACATGGTAAGAGAGCTTCAAGTCAAGTTCAGAGCTTACTATTAATGTTGATCCCAACG 644
 QY 598 GATATAACAAGCCACAGCAAGACTATACATGTTGAGCAGATGAAAGAACCCAGAGGA 657
 DB 645 GATATAACAAGCCACAGCAAGACTATACATGTTGAGCAGATGATGAAAGAACCCAGAGGA 704
 QY 658 CGCCACCATCTGTTCTCTTTA 677
 DB 705 CGCCACCATCTGTTCAATTA 724
 RESULT 14
 AAD03618 standard; cDNA; 876 BP.
 ID AAD03618;
 XX
 AC AAD03618;
 XX
 DT 11-SBP-2003 (revised)
 DT 19-JUN-2001 (first entry)
 XX
 DE Discosoma sp. magenta chromo/fluorescent protein, dmfp592 (NFP-9) cDNA.
 XX
 KW Anthozoa; Chromoprotein; fluorescent protein; dmfp592, NFP-9; sunsreen;
 KW analyte detection assay; selectable marker; recombinant DNA application;
 KW biosensor; pH indicator; invivo marker; selective filter; ss.
 XX
 OS Discosoma sp; magenta.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..737
 FT /tag= a
 FT /product= "Chromo/fluorescent protein, dmfp592 (NFP-9)"
 PN WO200127150-A2.
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028477.
 XX
 PR 14-OCT-1999; 99US-00418529.
 PR 15-OCT-1999; 99US-00418917.
 PR 15-OCT-1999; 99US-00418922.
 PR 19-NOV-1999; 99US-00444338.
 PR 19-NOV-1999; 99US-00444341.
 PR 09-DEC-1999; 99US-00457556.
 PR 09-DEC-1999; 99US-00457898.
 PR 09-DEC-1999; 99US-00458144.
 PR 09-DEC-1999; 99US-00458477.
 PR 10-DEC-1999; 99MO-US029405.
 PR 14-JUN-2000; 2000US-0211607P.
 PR 14-JUN-2000; 2000US-0211609P.
 PR 14-JUN-2000; 2000US-0211626P.
 PR 14-JUN-2000; 2000US-0211627P.
 PR 14-JUN-2000; 2000US-0211687P.

Sequence 876 BP; 256 A; 165 C; 232 G; 223 T; 0 U; 0 Other;

Query Match 83.5%; Score 566.4; DB 7; Length 876;

Best Local Similarity 90.6%; Pred. No. 8.3e-172;

Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

```
QY 1 ATGAGCTCTCCAGAAATGTTATCAAGAGCTTCATGAGCTTTAAAGTTCCGATGGAAGGA 60
   |||||
Db 45 ATGAGTTGTTCCAGAAATGATCAAGAGATTCATGAGTTCAAGGTTCCGATGGAAGGA 104
   |||||
QY 61 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAAGGAGGAGGAGGCCATACGAAGGC 120
   |||||
Db 105 ACCGTCATGGGCGACGAGTTTGAATAGAGCGAAGGAGGAGGCCATACGAAGGT 164
   |||||
QY 121 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180
   |||||
Db 165 CACTGTTCCGTAAGCTTATGATGTAACCAAGGGTGACCTTTGCCATTTGCTTGAATATT 224
   |||||
QY 181 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTATATGTCAAGCACCTGCCGACATACCA 240
   |||||
Db 225 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTATATGTCAAAACACCTGCCGACATACCA 284
   |||||
QY 241 GACTATAAAGCTGTCAATTTCTGGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 300
   |||||
Db 285 GACTATAAAGCTGTCAATTTCTGGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 344
   |||||
QY 301 GACGGTGGCGTCTGTAAGTAAACCAAGATTCAGTTTGCAAGATGGCTGTTTCATCTAC 360
   |||||
Db 345 GACGGTGGCGTCTGTAAGTAAACCAAGATTCAGTTTGCAAGATGGCTGTTTCATCTAC 404
   |||||
QY 361 AAGGTCAAGTTCAATGGCGTGAATCTTCCGATGAGCTGTTATGCAAAAGAGACA 420
   |||||
Db 405 GAGGTCAAGTTCAATGGCGTGAATCTTCCGATGAGCTGTTATGCAAGAGAGACA 464
   |||||
QY 421 ATGGGCTGGGAGCGACAGCTGAGCGTTTGTATCTGATGAGCGTGTGAAAGGAGAG 480
   |||||
Db 465 CGGGGCTGGGAGCGACAGCTGAGCGTTTGTATCTGATGAGCGTGTGAAAGGAGAGAC 524
   |||||
QY 481 ATTCAATAAGCTCTGAAGCTGAAGAAGCGTGTGCTATTACCTAGTTGAATTCAAAAGTATT 540
   |||||
Db 525 ATCCATATGGCTCTGAAGCTGAAGAAGGCGGCATTACCTCGTTGAATTCAAAAGTATT 584
   |||||
QY 541 TACATGGCAAGAAGCCT---GTGCACTTACAGGGTACTACTATGTTGACTCCAAACTG 597
   |||||
Db 585 TACATGGTAAAGAGCCTTCAAGTCAAGGCTACTATTAATGTTGACTCCAAACTG 644
   |||||
QY 598 GATATTAACAAGCAACAAGAAAGTATACAAATGTTGAGCATATGAAGAACCGAGGGA 657
   |||||
Db 645 GATATGACGAGCCACAAGAAATTACAGTGTGAGCATATGAAAAAACCCAGGGGA 704
   |||||
QY 658 CGCCACCATCTGTTCTTTA 677
   |||||
Db 705 CGCCACCATCTGTTCTTTA 724
   |||||
```

Search completed: July 11, 2004, 10:00:29
Job time : 309 secs

This Page Blank (uspto)